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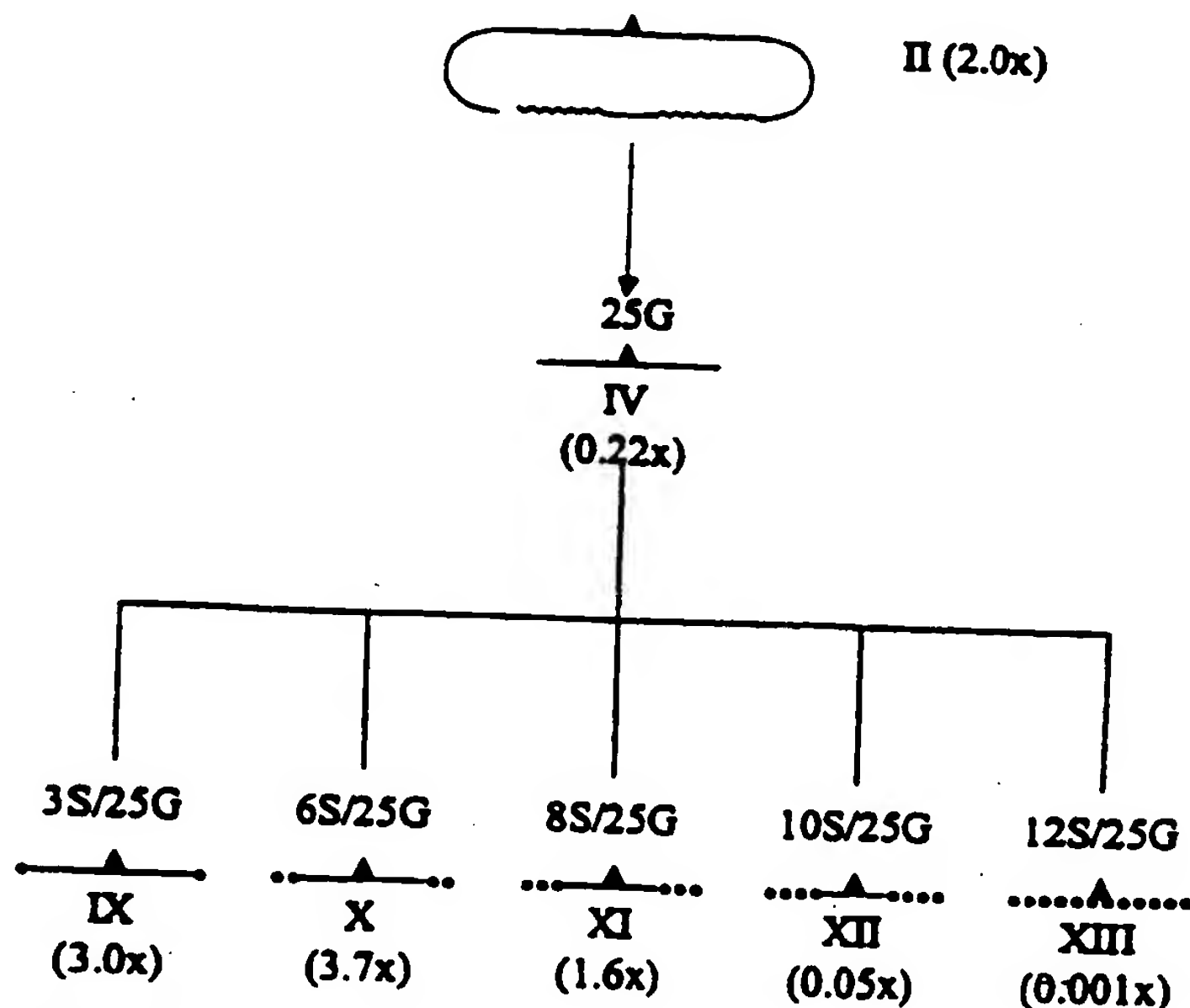
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(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS WITH MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES



(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations using modified single-stranded oligonucleotides. The oligonucleotides of the invention have at least one modified single-stranded oligonucleotides. The oligonucleotides of the invention have at least one modified nuclease-resistant terminal region comprising phosphorothioate linkages, LNA analogs or 2'-O-Me base analogs.

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TARGETED CHROMOSOMAL GENOMIC ALTERATIONS WITH MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Field Of The Invention

The technical field of the invention is oligonucleotide-directed repair or alteration of genetic information using novel chemically modified oligonucleotides. Such genetic information is preferably from a eukaryotic organism, i.e. a plant, animal or fungus.

Background Of The Invention

A number of methods have been developed specifically to alter the sequence of an isolated DNA in addition to methods to alter directly the genomic information of various plants, fungi and animals, including humans ("gene therapy"). The latter methods generally include the use of viral or plasmid vectors carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. For example, retroviral vectors containing a transgenic DNA sequence allowing for the production of a normal CFTR protein when administered to defective cells are described in U.S. Patent 5,240,846. Others have developed different "gene therapy vectors" which include, for example, portions of adenovirus (Ad) or adeno-associated virus (AAV), or other viruses. The virus portions used are often long terminal repeat sequences which are added to the ends of a transgene of choice along with other necessary control sequences which allow expression of the transgene. See U.S. Patents 5,700,470 and 5,139,941. Similar methods have been developed for use in plants. See, for example, U.S. Patent 4,459,355 which describes a method for transforming plants with a DNA vector and U.S. Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene vectors in any eukaryotic organism adds one or more exogenous copies of a gene, which gene may be foreign to the host, in a usually random fashion at one or more integration sites of the organism's genome at some frequency. The gene which was originally present in the genome, which may be a normal allelic variant, mutated, defective, and/or functional, is retained in the genome of the host.

These methods of gene correction are problematic in that complications which can compromise the health of the recipient, or even lead to death, may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. Another problem with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, viral or other vector remnants, control sequences required to allow production of the transgene protein, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. Other problems associated with these types of traditional gene therapy methods include autoimmune suppression of cells expressing an inserted gene due to the presence of foreign antigens. Concerns have also been raised with consumption, especially by humans, of plants containing exogenous genetic material.

More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant or animal genomes. See, for example, WO 99/07865 and U.S. Patent 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene conversion, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result compromises the utility of such a molecule in methods designed to alter the genomes of plants and animals, including in human gene therapy applications.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of

these oligonucleotides for directing gene conversion is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Early experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide with no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in the examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

Artificial chromosomes can be useful for the screening purposed identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large genomic DNA to be modified and used for generating transgenic animals [Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat. Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)]. Other vectors also have been developed for the cloning of large segments of mammalian DNA, including cosmids, and bacteriophage P1 [Stenberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)]. YACs have certain advantages over these alternative large capacity cloning vectors [Burke et al., Science, 236:806-812 (1987)]. The

maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert for a YAC.

An alternative to YACs are *E. coli* based cloning systems based on the *E. coli* fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) [Mejia et al., *Genome Res.* 7:179-186 (1997); Shizuya et al., *Proc. Natl. Acad. Sci.* 89:8794-8797 (1992); Ioannou et al., *Nat. Genet.* 6:84-89 (1994); Hosoda et al., *Nucleic Acids Res.* 18:3863 (1990)]. BACs are based on the *E. coli* fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. Furthermore, the PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis [Birnboim et al., *Nucleic Acids Res.* 7:1513-1523 (1979)].

Oligonucleotides designed for use in the alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants, fungi and animals are identified and the efficiency of alteration is analyzed both in vitro using a cell-free extract assay and in vivo using a yeast cell system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site

specific alteration of DNA is not only useful for studying function of proteins in vivo, but it is also useful for creating animal models for human disease, and in gene therapy. As described herein, oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA cells. The target DNA can be normal, cellular chromosomal DNA, extrachromosomal DNA present in cells in different forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing human DNA can be obtained from a variety of sources, including, e.g., the Whitehead Institute, and are described, e.g., in Cohen et al., Nature 336:698-701 (1993) and Chumakov, et al., Nature 377:174-297 (1995). The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex.

The low efficiency of gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., J. Am. Chem. Soc., 120:13252-3), we have found that it is not possible to predict which of any particular known modification would be most useful for any given alteration event, including for the construction of gene conversion oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See priority applications incorporated herein in their entirety; see also Gamper et al., Nucleic Acids Research 28: 4332-4339 (2000). We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748 and Wengel, WO 00/66604; also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical

modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different organisms or strains, or testing cells derived from different organisms or strains, or cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an in vitro gene repair assay. Similar results are also observed in vivo using yeast, mammalian, rodent, monkey, human and embryonic cells, including stem cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

Detailed Description Of The Invention

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration, including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity.

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-

DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligonucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Oligonucleotides of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cultured cells of human liver, lung, colon, cervix, kidney, epithelium and cancer cells and in monkey, hamster, rat and mouse cells of different types, as well as embryonic stem cells. Cells for use in the invention include, e.g., fungi including *S. cerevisiae*, *Ustilago maydis* and *Candida albicans*, mammalian, mouse, hamster, rat, monkey, human and embryonic cells including stem cells. The DNA domain is preferably fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration or conversion events. On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. These oligonucleotides are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA, phosphorothioate linkages, or 2'-O-methyl analog

incorporation into an oligonucleotide can not yet be predicted because the proteins involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, correcting oligonucleotides of defined sequence are provided for correction of genes mutated in human diseases. In the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for correction of human diseases contain phosphorothioate linkages, 2'-O-methyl analogs or LNAs or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs, phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4

analogues are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substrate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desired change. The oligonucleotides of the invention in different embodiments can alter DNA one, two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For

example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either the Watson or the Crick strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene repair activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the same sequence alteration. Similarly,

molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, more preferably, by using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (<http://www.idtdna.com>); this program is available for use on the world wide web at

<http://www.idtdna.com/program/oligoanalyzer/>

[oligoanalyzer.asp](http://www.idtdna.com/program/oligoanalyzer/).

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420 (<http://www.dnastar.com/products/PrimerSelect.html>).

If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e.

the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. According to certain preferred embodiments of the present invention, the isolated cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Modified cells may then be reintroduced into the organism as, for example, in bone marrow having a targeted gene. Alternatively, modified cells may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place in vivo following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the

genetic complement of the organism. Such agents may, for example, be used to develop plants or animals with improved traits by rationally changing the sequence of selected genes in cultured cells. Modified cells are then cloned into whole plants or animals having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated hererin by reference. Such plants or animals produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of transgenic animals having particular modified or inactivated genes. Altered animal or plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used for gene therapy to correct mutations causative of human diseases.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures as a pharmaceutical composition adapted for bathing cells in culture, for microinjection into cells in culture, and for intravenous administration to human beings or animals. Typically, compositions for cellular administration or for intravenous administration into animals, including humans, are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anaesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients will be supplied either separately or mixed together in unit dosage form, for example, as a dry, lyophilized powder or water-free concentrate. The composition may be stored in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent in activity units. Where the composition is administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade "water for injection" or saline. Where the composition is to be administered by injection, an ampule of sterile water for injection or saline may be provided so that the ingredients may be mixed prior to administration.

Pharmaceutical compositions of this invention comprise the compounds of the present invention and pharmaceutically acceptable salts thereof, with any pharmaceutically acceptable ingredient, excipient, carrier, adjuvant or vehicle.

The oligonucleotides of the invention are preferably administered to the subject in the form of an injectable composition. The composition is preferably administered parenterally, meaning intravenously, intraarterially, intrathecally, interstitially or intracavitarily. Pharmaceutical compositions of

this invention can be administered to mammals including humans in a manner similar to other diagnostic or therapeutic agents. The dosage to be administered, and the mode of administration will depend on a variety of factors including age, weight, sex, condition of the subject and genetic factors, and will ultimately be decided by medical personnel subsequent to experimental determinations of varying dosage as described herein. In general, dosage required for correction and therapeutic efficacy will range from about 0.001 to 50,000 $\mu\text{g/kg}$, preferably between 1 to 250 $\mu\text{g/kg}$ of host cell or body mass, and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an addition reagent or article of manufacture. The additional reagent or article of manufacture may comprise a cell extract, a cell, or a plasmid, such as one of those disclosed in the Figures herein, for use in an assay of the invention.

Brief Description Of The Drawings

Figure 1. Flow diagram for the generation of modified single-stranded oligonucleotides.

The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^{r} in the HUH7 cell extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^{r} gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA

residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

Figure 2. Genetic readout system for correction of a point mutation in plasmid pK^sm4021.

A mutant kanamycin gene harbored in plasmid pK^sm4021 is the target for correction by oligonucleotides. The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides. (A) Plasmid pT^sΔ208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. DNA sequences of representative kan^r colonies. Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. Gene correction in HeLa cells. Representative oligonucleotides of the invention are co-transfected with the pCMVneo(+)FIAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function..

Figure 8. *Oligonucleotides for correction of hygromycin resistance gene.* The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. *pAURNeo(-)FIAsH plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

Figure 10. *pYESHyg(x)eGFP plasmid.* This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

EXAMPLE 1

Assay Method For Base Alteration And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK^sm4021 (Figure 2) or the tetracycline gene of pT^sΔ208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored

when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURN δ o(-)FIAsH (Figure 9), bearing the kan^s gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase (kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FIAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FIAsH fusion product (after alteration) or the truncated Neo-/FIAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy. Additional constructs can be made to test additional gene alteration events.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137 \rightarrow G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHygEGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'-GACCTATCCACGCCCTCC-3'), Hyg Δ r (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrefp (5'-CTGGGATAGGTCCTGCGG-3'), Hyg Δ f (5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCTGCGG-3'), respectively to primer HygEGFP_r (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 μ g of vector pHygEGFP and 5 μ g of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4

DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper *et al.*, *Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 $\mu\text{g/ml}$ per A_{260} unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

Cell-free extracts. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately 2×10^8 cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM MgCl_2 ; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000xg. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage. We then immediately aliquote and freeze the supernatant at -80°C . We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C . We then centrifuge the cultures at 5000xg, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000xg for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000xg for 15 minutes. We then add glycerol to the clarified extract to a

concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 μ l are used, consisting of 10-30 μ g protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 μ g chimeric double-hairpin oligonucleotide or 0.55 μ g single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 μ g of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM MgCl₂, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 μ l H₂O, and is stored at -20°C. 5 μ l of plasmid from the resuspension (~100 ng) was transfected in 20 μ l of DH10B cells by electroporation (400 V, 300 μ F, 4 k Ω) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 μ g/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 μ l SOC. 200 μ l is added undiluted to each of two kanamycin (50 μ g/ml) agar plates and 200 μ l of a 10⁵ dilution is added to an ampicillin (100 μ g/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an Accucount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10⁻⁵ to correct for the amp dilution.

The following procedure can also be used. 5 μ l of resuspended reaction mixtures (total volume 50 μ l) are used to transform 20 μ l aliquots of electro-competent Δ H10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50 μ g/ml kanamycin or 12 μ g/ml tetracycline is added for an additional 3 hours. Prior to plating, the bacteria are pelleted and resuspended in 200 μ l of SOC. 100 μ l aliquots are plated onto kan or tet agar plates and 100 μ l of a 10⁻⁴ dilution of the cultures are concurrently plated on agar plates containing 100 μ g/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G-C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively

contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the exemplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

Correction of a mutant kanamycin gene in cultured mammalian cells. The experiments are performed using different mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO₂ in a humidified incubator to a density of 2×10^5 cells/ml in an 8 chamber slide (Lab-Tek). After replacing the regular DMEM with OptiMem, the cells are co-transfected with 10 µg of plasmid pAURNeo(-)FIAsH and 5 µg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 µg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FIAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FIAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for

example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid pkan^sm4021 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTet Δ 208. Table 4 illustrates data from repair of the pkan^sm4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^sm4021 contains a mutation (T-G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli*. This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of

plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the *kan^s* mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the *kan^s* mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

Frame shift mutations are repaired. By using plasmid pT^sΔ208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more

subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^sm4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence TTCGATAAGCCTATGCTGACCCGTG corrects the original mutation present in the kanamycin resistance gene of pK^sm4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence TTCGGCTACGACTGGGCACAACAGACAATTGGC with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK^sm4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^sM4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-

TTGTGCCCAGTCGTATCCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGAA TAGCCTCTCCACCCAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-

GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCAATTGTCTGTTGTGCCCAGTCGTAGCCGAAT AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK^sm4021 by monitoring kanamycin resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to

determine whether the additional, silent alteration has also been introduced. The results of an analysis are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

Nuclease sensitivity of unmodified DNA oligonucleotide. Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM MgCl₂; 10 mM DTT; 10% [v/v] glycerol; and 1 % [w/v] PVP). We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000xg for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan ^r colonies	Fold increase
I	pK ^S m4021	10	300	
I		20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
-		20	0	
I		-	0	

Plasmid pK^Sm4021 (1μg), the indicated oligonucleotide (1.5 μg chimeric oligonucleotide or 0.55 μg single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 μg of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan^r colonies counted. The data represent the number of kanamycin resistant colonies per 10⁶ ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan^r colonies (second reaction) and in all reactions was calculated using the 20µg sample.

Table II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A. Oligonucleotide	Plasmid	Extract	kan ^r colonies
IX (3S/25G)	↓	HUH7	637
X (6S/25G)		HUH7	836
IX		MEF2 ^{-/-}	781
X		MEF2 ^{-/-}	676
IX		MEF3 ^{-/-}	582
X		MEF3 ^{-/-}	530
IX		MEF ^{+/+}	332
X		MEF ^{+/+}	497
-		MEF2 ^{-/-}	10
-		MEF3 ^{-/-}	5
-		MEF ^{+/+}	14

Chimeric oligonucleotide (1.5 µg) or modified single-stranded oligonucleotide (0.55 µg) was incubated with 1 µg of plasmid pK^m4021 and 20 µg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 (2^{-/-}) or MSH3 (3^{-/-}) deleted. MEF^{+/+} indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10⁶ ampicillin resistant colonies.

Table III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	tet ^r colonies
Tet IX (3S/25A; 0.5 µg)	pT ^s Δ208 (1µg)	-	0
	↓	20µg	0
Tet IX (0.5 µg)		↓	48
Tet IX (1.5 µg)			130
Tet IX (2.0 µg)			68
Tet I (chimera; 1.5 µg)	↓	↓	48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide.

The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10⁶ ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT^sΔ208. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan ^r colonies
II (chimera)	pK ^S m4021	30µg Canola	337
IX (3S/25G)	↓	Canola	763
X (6S/25G)		Canola	882
II		<i>Musa</i>	203
IX		<i>Musa</i>	343
X		<i>Musa</i>	746
-		Canola	0
-		<i>Musa</i>	0
IX		- Canola	0
X		- <i>Musa</i>	0

Canola or *Musa* cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 µg) and modified single-stranded oligonucleotides IX and X (0.55µg) were used to correct pK^Sm4021. Total number of kan^r colonies are present per 10⁷ ampicillin resistant colonies and represent an average of four independent experiments.

Table V

Gene repair activity in cell-free extracts prepared from yeast (Saccharomyces cerevisiae)

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	kan' /amp' x 10 ⁶
Wild type	pKan'm4021	1µg		0.36
Wild type	↓		1µg	0.81
ΔRAD52		1µg		10.72
ΔRAD52			1µg	17.41
ΔPMS1		1µg		2.02
ΔPMS1			1µg	3.23

In this experiment, the kan' gene in pKan'4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/25G).

EXAMPLE 2

Yeast Cell Targeting Assay Method for Base Alteration and Preferred Oligonucleotide Selection

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137 \rightarrow G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μ g pAUR123 vector DNA, as well as, 10 μ g of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74 α , is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence. Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2-O-methylated modified oligonucleotide may be used as a control.

Oligonucleotide synthesis and cells. We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 MAT α at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD₆₀₀ was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 μ l 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 μ l of cells with 5 μ g of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 μ F, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200 μ l of this culture on selective plates containing 300 μ g/ml hygromycin and spread 200 μ l of a 10⁵ dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10⁵ aureobasidinA resistant colonies.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in

Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-

CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGG**TAC**GCCTGCGGGTAAATAGCTGCGCCGATG
GTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-

CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGAT**AC**GCCTGCGGGTAA**AC**AGCTGCGCCGATG
GTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-

CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGAT**AC**GCCTGCGGGTAAATAGCTGCGCCG**AC**G
GTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other

oligonucleotides of the invention.

Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74 α , with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6 μ g, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74 α and HygE3T/74). Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74 α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution

mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74 α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74 α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μ g. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10 ⁵)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.

Oligonucleotide Tested (5 µg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74 α	1464	2248
Kan70T	0	0

Table 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (µg)	Colonies on hygromycin	Colonies on aureobasidin (/10 ⁵)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

Example 3 Cultured Cell Manipulation

Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34⁺ cells are immunomagnetically purified from mononuclear cells using either the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin⁻CD38⁻ cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA).

Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection. S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 μ g/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 μ g/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 μ g/ml low-density lipoprotein (LDL; Sigma; St. Louis, MO), 50 mM HEPES buffer and 50 μ M 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 μ g/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 μ to 0.3 μ outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are fluorescently labeled allow determination of the amount of oligonucleotide delivered to the cells.

For in vitro erythropoiesis from Lin⁻CD38⁻ cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythroid progeny. CD34⁺ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β -globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phosphate precipitation, or any other method known in the art.

Notes on the tables presented below:

Each of the following tables presents, for the specified human gene, a plurality of mutations that are known to confer a clinically-relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the human genome according to the present invention.

The left-most column identifies each mutation and the clinical phenotype that the mutation confers.

For most entries, the mutation is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Codon numbering is according to the Human Gene Mutation Database, Cardiff, Wales, UK (<http://archive.uwcm.ac.uk/search/mg/allgenes>). Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the human genome or in cloned human DNA including human DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

EXAMPLE 4

Adenosine Deaminase (ADA)

Adenosine deaminase (ADA, EC 3.5.4.4) catalyses the deamination of adenosine and 2'-deoxyadenosine to inosine or 2'-deoxyinosine respectively. ADA deficiency has been identified as the metabolic basis for 20-30% of cases with recessively inherited severe combined immunodeficiency (SCID). Affected infants are subject to recurrent chronic viral, fungal, protozoal, and bacterial infections and frequently present with persistent diarrhea, failure to thrive and candidiasis. In patients homozygous for ADA deficiency, 2'-deoxyadenosine accumulating during the rapid turnover of cells rich in DNA is converted back to dATP, either by adenosine kinase or deoxycytidine kinase. Many hypotheses have been advanced to explain the specific toxicity to the immune system in ADA deficiency. The apparently selective accumulation of dATP in thymocytes and peripheral blood B cells, with resultant inhibition of ribonucleotide reductase and DNA synthesis is probably the principal mechanism.

The structural gene for ADA is encoded as a single 32 kb locus containing 12 exons. Studies of the molecular defect in ADA-deficient patients have shown that mRNA is usually detectable in normal or supranormal amounts. Specific base substitution mutations have been detected in the majority of cases with the complete deficiency. A C-to-T base substitution mutation in exon 11 accounts for a high proportion of these, whilst a few patients are homozygous for large deletions encompassing exon I. A common point mutation resulting in a heat-labile ADA has been characterised in some patients with partial ADA deficiency, a disorder with an apparently increased prevalence in the Caribbean.

As yet no totally effective therapy for ADA deficiency has been reported, except in those few cases where bone marrow from an HLA/MLR compatible sibling donor was available.

Two therapeutic approaches have provided long-term benefit in specific instances. First, reconstitution using T cell depleted mismatched sibling marrow has been encouraging, particularly in early presenters completely deficient in ADA. Secondly, therapy with polyethylene glycol-modified adenosine deaminase (PEG-ADA) for more than 5 years has produced a sustained increase in lymphocyte numbers and mitogen responses together with evidence of in vivo B cell function. Success has generally been achieved in late presenters with residual ADA activity in mononuclear cells.

ADA deficiency has been chosen as the candidate disease for gene replacement therapy and the first human experiment commenced in 1990. The clinical consequences of overexpression of ADA activity - one of the potential hazards of gene implant - are known and take the form of an hereditary haemolytic anaemia associated with a tissue-specific increase in ADA activity. The genetic basis for the

latter autosomal dominant disorder seemingly relates to markedly increased levels of structurally normal ADA mRNA.

Table 10
ADA Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency GLN3TERM CAG to TAG	AGAGACCCACCGAGCGGCGGCGGAGGGAGCAGCGCCGGGG CGCACGAGGGCACCATGGCCAGACGCCCGCCTTCGACAAG CCCAAAGTGAGCGCGCGCGGGGGCTCCGGGGACGGGGGTC	1
	GACCCCGTCCCCGGAGCCCCGCGCGCGCTCACTTTGGG CTTGTCGAAGGCGGGCGTCTGGGCCATGGTGCCCTCGTGCG CCCCGGCGCTGCTCCCTCCGCCCGCTCGGTGGGTCTCT	2
	CCATGGCCCAGACGCCC	3
	GGGCGTCTGGGCCATGG	4
Adenosine deaminase deficiency HIS15ASP CAT to GAT	TATTTGTTCTCTCTCTCCCTTTCTCTCTCTTCCCCCTGCCC CCTTGCAGGTAGAACTGCATGTCCACCTAGACGGATCCATCA AGCCTGAAACCATCTTATACTATGGCAGGTAAGTCC	5
	GGACTTACCTGCCATAGTATAAGATGGTTTCAGGCTTGATGGA TCCGTCTAGGTGGACATGCAGTTCTACCTGCAAGGGGGCAG GGGAAGAGAGAGAGAAAGGGAGAGAGAGAAACAATA	6
	TAGAACTGCATGTCCAC	7
	GTGGACATGCAGTTCTA	8
Adenosine deaminase deficiency GLY20ARG GGA to AGA	TCCCTTTCTCTCTCTTCCCCCTGCCCCCTTGCAGGTAGAA CTGCATGTCCACCTAGACGGATCCATCAAGCCTGAAACCATC TTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCT	9
	AGGGCTCTTCTGTATGGACTTACCTGCCATAGTATAAGATGGT TTCAGGCTTGATGGATCCGTCTAGGTGGACATGCAGTTCTAC CTGCAAGGGGGCAGGGGGAAGAGAGAGAGAAAGGGA	10
	ACCTAGACGGATCCATC	11
	GATGGATCCGTCTAGGT	12
Adenosine deaminase deficiency GLY74CYS GGC to TGC	CCTGGAGCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACC CCTTTCTTCCCTTCCCAGGGGCTGCCGGGAGGCTATCAAAAG GATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGG	13

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCTCTTTGGCCTTCATCTCTACAACTCATAGGCGATCCTTTT GATAGCCTCCCGGCAGCCCTGGGAAGGGAAGAAAGGGGTT GGGAACAACCTTCCCAAGTCCCTTGGGAGCTCCAGG	14
	CTATCGCGGGCTGCCGG	15
	CCGGCAGCCCGCGATAG	16
Adenosine Deaminase Deficiency ARG76TRP CGG to TGG	GCTCCAAGGGACTTGGGGAAGGTTGTTCCAACCCCTTTCT TCCCTTCCAGGGGCTGCCGGGAGGCTATCAAAGGATCGC CTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGG	17
	CCACGCCCTCTTTGGCCTTCATCTCTACAACTCATAGGCGAT CCTTTTGATAGCCTCCCGGCAGCCCTGGGAAGGGAAGAAA GGGGTTGGGAACAACCTTCCCAAGTCCCTTGGGAGC	18
	GGGGCTGCCGGGAGGCT	19
	AGCCTCCCGGCAGCCCC	20
Adenosine Deaminase Deficiency LYS80ARG AAA to AGA	TTGGGGAAGGTTGTTCCAACCCCTTTCTTCCCTTCCAGGG GCTGCCGGGAGGCTATCAAAGGATCGCCTATGAGTTTGTAG AGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGT	21
	ACCTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTACAA ACTCATAGGCGATCCTTTGATAGCCTCCCGGCAGCCCCTGG GAAGGGAAGAAAGGGGTTGGGAACAACCTTCCCCAA	22
	GGCTATCAAAGGATCG	23
	CGATCCTTTGATAGCC	24
Adenosine deaminase deficiency ALA83ASP GCC to GAC	GTTGTTCCAACCCCTTTCTTCCCTTCCAGGGGCTGCCGGG AGGCTATCAAAGGATCGCCTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGTATGTGGAGGTGCGGTACAG	25
	CTGTACCGCACCTCCACATACACCACGCCCTCTTTGGCCTTC ATCTCTACAACTCATAGGCGATCCTTTGATAGCCTCCCGGC AGCCCCTGGGAAGGGAAGAAAGGGGTTGGGAACAAC	26
	AAGGATCGCCTATGAGT	27
	ACTCATAGGCGATCCTT	28
Adenosine deaminase deficiency TYR97CYS TAT to TGT	AGGCTATCAAAGGATCGCCTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGTATGTGGAGGTGCGGTACAGTCCG CACCTGCTGGCCAACCTCAAAGTGGAGCCAATCCCCTG	29
	CAGGGGATTGGCTCCACTTTGGAGTTGGCCAGCAGGTGCGG ACTGTACCGCACCTCCACATACACCACGCCCTCTTTGGCCTT CATCTCTACAACTCATAGGCGATCCTTTGATAGCCT	30

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CGTGGTGTATGTGGAGG	31
	CCTCCACATACACCACG	32
Adenosine deaminase deficiency ARG101GLN CGG to CAG	GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA	33
	TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAACTCATAGGCGATCC	34
	GGAGGTGCGGTACAGTC	35
	GACTGTACCGCACCTCC	36
Adenosine deaminase deficiency ARG101LEU CGG to CTG	GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA	37
	TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAACTCATAGGCGATCC	38
	GGAGGTGCGGTACAGTC	39
	GACTGTACCGCACCTCC	40
Adenosine deaminase deficiency ARG101TRP CGG to TGG	AGGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGC GTGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGC CAACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTG	41
	CAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCCA GCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC TCTTTGGCCTTCATCTCTACAACTCATAGGCGATCCT	42
	TGGAGGTGCGGTACAGT	43
	ACTGTACCGCACCTCCA	44
Adenosine deaminase deficiency PRO104LEU CCG to CTG	ATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATG TGGAGGTGCGGTACAGTCCGCACCTGCTGGCCAACTCCAAA GTGGAGCCAATCCCCTGGAACCAGGCTGAGTGAGTGAT	45
	ATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCACTTTG GAGTTGGCCAGCAGGTGCGGACTGTACCGCACCTCCACATA CACCACGCCCTCTTTGGCCTTCATCTCTACAACTCAT	46
	GTACAGTCCGCACCTGC	47
	GCAGGTGCGGACTGTAC	48

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency LEU106VAL CTG to GTG	TTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAG GTGCGGTACAGTCCGCACCTGCTGGCCAACTCCAAAGTGGA GCCAATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCC	49
	GGCCCATCACTCACTCAGCCTGGTTCAGGGGATTGGCTCCA CTTTGGAGTTGGCCAGCAGGTGCGGACTGTACCGCACCTCC ACATACACCACGCCCTCTTTGGCCTTCATCTCTACAAA	50
	GTCCGCACCTGCTGGCC	51
	GGCCAGCAGGTGCGGAC	52
Adenosine deaminase deficiency LEU107PRO CTG to CCG	TAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGTG CGGTACAGTCCGCACCTGCTGGCCAACTCCAAAGTGAGGCC AATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCCTGGA	53
	TCCAGGCCCATCACTCACTCAGCCTGGTTCAGGGGATTGGC TCCACTTTGGAGTTGGCCAGCAGGTGCGGACTGTACCGCAC CTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTA	54
	GCACCTGCTGGCCAACT	55
	AGTTGGCCAGCAGGTGC	56
Adenosine deaminase deficiency PRO126GLN CCA to CAA	GCCTTCCTTTTGCCTCAGGCCCATCCCTACTCCTCTCCTCAC ACAGAGGGGACCTCACCCAGACGAGGTGGTGGCCCTAGTG GGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGT	57
	ACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCAC TAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGTGTG AGGAGAGGAGTAGGGATGGGCCTGAGGCAAAGGAAGGC	58
	CCTCACCCAGACGAGG	59
	CCTCGTCTGGGGTGAGG	60
Adenosine deaminase deficiency VAL129MET GTG to ATG	TTTGCCTCAGGCCCATCCCTACTCCTCTCCTCACACAGAGGG GACCTCACCCAGACGAGGTGGTGGCCCTAGTGGGCCAGGG CCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC	61
	GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC TGGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCC TCTGTGTGAGGAGAGGAGTAGGGATGGGCCTGAGGCAA	62
	CAGACGAGGTGGTGGCC	63
	GGCCACCACCTCGTCTG	64

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency GLY140GLU GGG to GAG	ACAGAGGGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTG GGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCA AGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAG	65
	CTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTT GACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCCA CTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGT	66
	GCAGGAGGGGGAGCGAG	67
	CTCGCTCCCCCTCCTGC	68
Adenosine deaminase deficiency ARG142GLN CGA to CAA	GGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCAG GGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC GGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTA	69
	TACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCG GGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCT GGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCC	70
	GGGGGAGCGAGACTTCG	71
	CGAAGTCTCGCTCCCCC	72
Adenosine deaminase deficiency ARG142TERM CGA to TGA	GGGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCA GGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC CGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGT	73
	ACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGG GCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTG GCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCC	74
	AGGGGGAGCGAGACTTC	75
	GAAGTCTCGCTCCCCCT	76
Adenosine deaminase deficiency ARG149GLN CGG to CAG	TGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCG AGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATGC GCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCAGGG	77
	CCCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCG CATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTC GCTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCA	78
	CAAGGCCCGGTCCATCC	79
	GGATGGACCGGGCCTTG	80

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency ARG149TRP CGG to TGG	GTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGC GAGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATG CGCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCCAGG	81
	CCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCGC ATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTCG CTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCAC	82
	TCAAGGCCCGGTCCATC	83
	GATGGACCGGGCCTTGA	84
Adenosine deaminase deficiency LEU152MET CTG to ATG	CTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCG GGGTCAAGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAG CCCAGTGAGTAGGATCACCGCCCTGCCAGGGCCGCCCGT	85
	ACGGGCGGCCCTGGGCAGGGCGGTGATCCTACTCACTGGG CTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTTGACCC CGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCCACTAG	86
	GGTCCATCCTGTGCTGC	87
	GCAGCACAGGATGGACC	88
Adenosine deaminase deficiency ARG156CYS CGC to TGC	GGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCCG GGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTAG GATCACCGCCCTGCCAGGGCCGCCCGTCTCACCCCTGGCC	89
	GGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGATC CTACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACC GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC	90
	GCTGCATGCGCCACCAG	91
	CTGGTGGCGCATGCAGC	92
Adenosine deaminase deficiency ARG156HIS CGC to CAC	GCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCCG GTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTAGG ATCACCGCCCTGCCAGGGCCGCCCGTCTCACCCCTGGCCC	93
	GGGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGAT CCTACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGAC CGGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGC	94
	CTGCATGCGCCACCAGC	95
	GCTGGTGGCGCATGCAG	96

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Adenosine deaminase deficiency VAL177MET GTG to ATG	CTGCCCACAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAA GAAGTACCAGCAGCAGACCGTGGTAGCCATTGACCTGGCTG GAGATGAGACCATCCCAGGAAGCAGCCTCTTGCCTGGAC	97
	GTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCATCTCCAG CCAGGTCAATGGCTACCA C GGTCTGCTGCTGGTACTTCTTAC ACAGCTCCACCACCTTGGGGGACCAGTCTGTGGGCAG	98
	AGCAGACCGTGGTAGCC	99
	GGCTACCACGGTCTGCT	100
Adenosine deaminase deficiency ALA179ASP GCC to GAC	CAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAAGAAGTAC CAGCAGCAGACCGTGGTAGCATTGACCTGGCTGGAGATGA GACCATCCCAGGAAGCAGCCTCTTGCCTGGACATGTCCA	101
	TGGACATGTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCA TCTCCAGCCAGGTCAATGGCTACCACGGTCTGCTGCTGGTAC TTCTTACACAGCTCCACCACCTTGGGGGACCAGTCTG	102
	CGTGGTAGCCATTGACC	103
	GGTCAATGGCTACCACG	104
Adenosine deaminase deficiency GLN199PRO CAG to CCG	CCATTGACCTGGCTGGAGATGAGACCATCCCAGGAAGCAGC CTCTTGCCTGGACATGTCCAGGCCTACCAGGTGGGTCTGT GAGAAGGAATGGAGAGGCTGGCCCTGGGTGAGCTTGTCT	105
	AGACAAGCTCACCCAGGGCCAGCCTCTCCATTCTTCTCACA GGACCCACCTGGTAGGCCIGGACATGTCCAGGCAAGAGGCT GCTTCCTGGGATGGTCTCATCTCCAGCCAGGTCAATGG	106
	ACATGTCCAGGCCTACC	107
	GGTAGGCCTGGACATGT	108
Adenosine deaminase deficiency ARG211CYS CGT to TGT	GCTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGC TGTGAAGAGCGGCATTACCGTACTGTCCACGCCGGGGAGG TGGGCTCGGCCGAAGTAGTAAAGAGGTGAGGGCCTGGG	109
	CCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCACCT CCCCGGCGTGGACAGTACGGTGAATGCCGCTCTTCACAGCC TCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAGC	110
	GCATTCACCGTACTGTC	111
	GACAGTACGGTGAATGC	112

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency ARG211HIS CGT to CAT	CTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGCT GTGAAGAGCGGCATTACCGTACTGTCCACGCCGGGAGGT GGGCTCGGCCGAAGTAGTAAAGAGGTGAGGGCCTGGGC	113
	GCCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCCACC TCCCCGGCGTGGACAGTACGGTGAATGCCGCTCTTCACAGC CTCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAG	114
	CATTCACCGTACTGTCC	115
	GGACAGTACGGTGAATG	116
Adenosine deaminase deficiency ALA215THR GCC to ACC	ATGACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGG CATTACCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCG AAGTAGTAAAGAGGTGAGGGCCTGGGCTGGCCATGGGG	117
	CCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTACTTCGG CCGAGCCCACCTCCCCGGCGTGGACAGTACGGTGAATGCCG CTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGTCAT	118
	CTGTCCACGCCGGGGAG	119
	CTCCCCGGCGTGGACAG	120
Adenosine deaminase deficiency GLY216ARG GGG to AGG	ACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCAT TCACCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCGAAG TAGTAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCC	121
	GGACCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTACTT CGGCCGAGCCCACCTCCCCGGCGTGGACAGTACGGTGAATG CCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGT	122
	TCCACGCCGGGGAGGTG	123
	CACCTCCCCGGCGTGA	124
Adenosine deaminase deficiency GLU217LYS GAG to AAG	TGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCATTCA CCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCGAAGTAG TAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCCCTC	125
	GAGGGACCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTA CTTCGGCCGAGCCCACCTCCCCGGCGTGGACAGTACGGTGA ATGCCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCA	126
	ACGCCGGGGAGGTGGGC	127
	GCCCACCTCCCCGGCGT	128

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency THR233ILE ACA to ATA	CTGCCTCCTCCCATACTTGGCTCTATTCTGCTTCTCTACAGGC TGTGGACATACTCAAGACAGAGCGGCTGGGACACGGCTACC ACACCCTGGAAGACCAGGCCCTTTATAACAGGCTGCG	129
	CGCAGCCTGTTATAAAGGGCCTGGTCTTCCAGGGTGTGGTAG CCGTGTCCCAGCCGCTCTGTCTTGAGTATGTCCACAGCCTGT AGAGAAGCAGAATAGAGCCAAGTATGGGAGGAGGCAG	130
	ACTCAAGACAGAGCGGC	131
	GCCGCTCTGTCTTGAGT	132
Adenosine deaminase deficiency ARG253PRO CGG to CCG	CAGAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAG GCCCTTTATAACAGGCTGCGGCAGGAAAACATGCACTTCGAG GTAAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGC	133
	GCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACCTC GAAGTGCATGTTTTCTGCCGCAGCCTGTTATAAAGGGCCTG GTCTTCCAGGGTGTGGTAGCCGTGTCCAGCCGCTCTG	134
	CAGGCTGCCGCAGGAAA	135
	TTTCCTGCCGCAGCCTG	136
Adenosine deaminase deficiency GLN254TERM CAG to TAG	GAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAGGC CCTTTATAACAGGCTGCGGCAGGAAAACATGCACTTCGAGGT AAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGCTG	137
	CAGCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACC TCGAAGTGCATGTTTTCTGCCGCAGCCTGTTATAAAGGGCC TGGTCTTCCAGGGTGTGGTAGCCGTGTCCAGCCGCTC	138
	GGCTGCGGCAGGAAAAC	139
	GTTTTCTGCCGCAGCC	140
Adenosine deaminase deficiency PRO274LEU CCG to CTG	CCACACACCTGCTCTTCCAGATCTGCCCCTGGTCCAGCTACC TCACTGGTGCCTGGAAGCCGGACACGGAGCATGCAGTCATT CGGTGAGCTCTGTTCCCCTGGGCCTGTTCAATTTTGT	141
	AACAAAATTGAACAGGCCAGGGGAACAGAGCTCACCGAATG ACTGCATGCTCCGTGTCCGGCTTCCAGGCACCAGTGAGGTA GCTGGACCAGGGGCAGATCTGGAAGAGCAGGTGTGTGG	142
	CTGGAAGCCGGACACGG	143
	CCGTGTCCGGCTTCCAG	144

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency SER291LEU TCG to TTG	GGAGGCTGATTCTCTCCTCCTCCCTCTTCTGCAGGCTCAAAA ATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGCTCA TCTTCAAGTCCACCCTGGACACTGATTACCAGATGAC	145
	GTCATCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGC GGGTCATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTTTGA GCCTGCAGAAGAGGGAGGAGGAGAGAATCAGCCTCC	146
	TAACTACTCGCTCAACA	147
	TGTTGAGCGAGTAGTTA	148
Adenosine deaminase deficiency PRO297GLN CCG to CAG	CCTCCCTCTTCTGCAGGCTCAAAAATGACCAGGCTAACTACT CGCTCAACACAGATGACCCGCTCATCTTCAAGTCCACCCTGG AACTGATTACCAGATGACCAAACGGGACATGGGCTT	149
	AAGCCCATGTCCCGTTTGGTCATCTGGTAATCAGTGTCCAGG GTGGACTTGAAGATGAGCGGGTCATCTGTGTTGAGCGAGTAG TTAGCCTGGTCATTTTTGAGCCTGCAGAAGAGGGAGG	150
	AGATGACCCGCTCATCT	151
	AGATGAGCGGGTCATCT	152
Adenosine deaminase deficiency LEU304ARG CTG to CGG	AAAATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGC TCATCTTCAAGTCCACCCTGGACACTGATTACCAGATGACCAA ACGGGACATGGGCTTTACTGAAGAGGAGTTTAAAAG	153
	CTTTTAACTCCTCTTCAGTAAAGCCCATGTCCCGTTTGGTCA TCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGCGGGT CATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTT	154
	GTCCACCCCTGGACACTG	155
	CAGTGTCCAGGGTGGAC	156
Adenosine deaminase deficiency ALA329VAL C-to-T at base 1081	GCCTTCTTTGTTCTCTGGTTCCATGTTGTCTGCCATTCTGGCC TTTCCAGAACATCAATGCGGCCAAATCTAGTTTCCTCCCAGAA GATGAAAAGAGGGAGCTTCTCGACCTGCTCTATAA	157
	TTATAGAGCAGGTCGAGAAGCTCCCTCTTTTCATCTTCTGGGA GGAACTAGATTTGGCCGCATTGATGTTCTGGAAAGGCCAGA ATGGCAGACAACATGGAACCAGAGAACAAGAAGGC	158
	CATCAATGCGGCCAAAT	159
	ATTTGGCCGCATTGATG	160

EXAMPLE 5

P53 Mutations

The p53 gene codes for a protein that acts as a transcription factor and serves as a key regulator of the cell cycle. Mutation in this gene is probably the most significant genetic change characterizing the transformation of cells from normalcy to malignancy.

Inactivation of p53 by mutation disrupts the cell cycle which, in turn, sets the stage for tumor formation. Mutations in the p53 gene are among the most commonly diagnosed genetic disorders, occurring in as many as 50% of cancer patients. For some types of cancer, most notably of the breast, lung and colon, p53 mutations are the predominant genetic alternations found thus far. These mutations are associated with genomic instability and thus an increased susceptibility to cancer. Some p53 lesions result in malignancies that are resistant to the most widely used therapeutic regimens and therefore demand more aggressive treatment.

That p53 is associated with different malignant tumors is illustrated in the Li-Fraumeni autosomal dominant hereditary disorder characterized by familial multiple tumors due to mutation in the p53 gene. Affected individuals can develop one or more tumors, including: brain (12%); soft-tissue sarcoma (12%); breast cancer (25%); adrenal tumors (1%); bone cancer (osteosarcoma) (6%); cancer of the lung, prostate, pancreas, and colon as well as lymphoma and melanoma can also occur.

Certain of the most frequently mutated codons are codons 175, 248 and 273, however a variety of oligonucleotides are described below in the attached table.

Table 11
p53 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
In 2 families with Li-Fraumeni syndrome, there was a C-to-T mutation at the first nucleotide of codon 248 which changed arginine to tryptophan.	GACTGTACCACCATCCACTACAACATCATGTGTAACAGTTCCT GCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATC ACACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACC	161
	GGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGA TGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAA CTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTC	162
	GCATGAACCGGAGGCC	163

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGGCCTCC <u>G</u> GTTCATGC	164
In a family with the Li-Fraumeni syndrome, a G-to-A mutation at the first nucleotide of codon 258 resulting in the substitution of lysine for glutamic acid.	TGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCAT CCTCACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCAC TTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCCTC	165
	GAGGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGT GGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGAT GGGCCTCCGGTTCATGCCGCCCATGCAGGAAGTGTACA	166
	TCACACTGGAAGACTCC	167
	GGAGTCTTCCAGTGTGA	168
In a family with the Li-Fraumeni syndrome, a G-to-T mutation at the first nucleotide of codon 245 resulting in the substitution of cysteine for glycine.	GTTGGCTCTGACTGTACCACCATCCACTACAACACTACATGTGTA ACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTC ACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCA	169
A gly245-to-ser, GGC-to-AGC, mutation was found in a patient in whom osteosarcoma was diagnosed at the age of 18 years.	TGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGA TGGGCCTCCGGTTCATGCCGCCCATGCAGGAAGTGTACACA TGTAAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAAC	170
	GCATGGGCGGCATGAAC	171
	GTTCATGCCGCCCATGC	172
In a family with the Li-Fraumeni syndrome, a germline mutation at codon 252: a T-to-C change at the second position resulted in substitution of proline for leucine.	TCCACTACAACACTACATGTGTAACAGTTCCTGCATGGGCGGCA TGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACT CCAGGTCAGGAGCCACTTGCCACCCTGCACACTGGCC	173
	GGCCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTC TTCCAGTGTGATGATGGTGAGGATGGGCCTCCGGTTCATGCC GCCCATGCAGGAAGTGTACACATGTAGTTGTAGTGGA	174
	GCCCATCCTCACCATCA	175
	TGATGGTGAGGATGGGC	176

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
<p>Researchers analyzed for mutations in p53 hepatocellular carcinomas from patients in Qidong, an area of high incidence in China, in which both hepatitis B virus and aflatoxin B1 are risk factors. Eight of 16 tumors had a point mutation at the third base position of codon 249. The G-to-T mutation at codon 249 led to a change from arginine to serine (AGG to AGT).</p>	<p>TACCACCATCCACTACAACATGTGTAAACAGTTCCTGCATG GGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACT GGAAGACTCCAGGTCAGGAGCCACTTGCCACCCTGCA</p>	177
	<p>TGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTG TGATGATGGTGAAGATGGGCTCCGGTTCATGCCGCCCATG CAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTA</p>	178
	<p>AACCGGAGGCCCATCCT</p>	179
	<p>AGGATGGGCTCCGGTT</p>	180
<p>In cases of hepatocellular carcinoma in southern Africa, a G-to-T substitution in codon 157 resulting in a change from valine to phenylalanine.</p>	<p>CTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACA CCCCGCCCCGGCACC CGCTCCGCGCCATGGCCATCTACAA GCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCC</p>	181
	<p>GGCAGCGCCTCACAACTCCGTCATGTGCTGTGACTGCTTGT AGATGGCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGT GGAATCAACCCACAGCTGCACAGGGCAGGTCTTGCCAG</p>	182
	<p>GCACCCGCGTCCGCGCC</p>	183
	<p>GGCGCGGACGCGGGTGC</p>	184
<p>In a family with Li-Fraumeni in which noncancerous skin fibroblasts from affected individuals showed an unusual radiation-resistant phenotype, a point mutation in codon 245 of the P53 gene. A change from GGC to GAC predicted substitution of aspartic acid for glycine.</p>	<p>TTGGCTCTGACTGTACCACCATCCACTACAACATGTGTAA CAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCA CCATCATCACACTGGAAGACTCCAGGTCAGGAGCCAC</p>	185
	<p>GTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGG ATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACAC ATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAA</p>	186
	<p>CATGGGCGGCATGAACC</p>	187
	<p>GGTTCATGCCGCCCATG</p>	188

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
In 2 of 8 families with Li-Fraumeni syndrome, a mutation in codon 248: a CGG-to-CAG change resulting in substitution of glutamine for arginine.	ACTGTACCACCATCCACTACAACATCATGTGTAAACAGTTCCTG CATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCA CACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACCC	189
	GGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGAT GATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGG AACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGT	190
	CATGAACCGGAGGCCCA	191
	TGGGCCTCCGGTTCATG	192
In 9 members of an extended family with Li-Fraumeni syndrome, a germline mutation at codon 133 (ATG-to-ACG), resulted in the substitution of threonine for methionine (M133T), and completely cosegregated with the cancer syndrome.	CCCTGACTTTCAACTCTGTCTCCTTCCTCTTCTACAGTACTC CCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACCTG CCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCC	193
	GGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGT CTTGGCCAGTTGGCAAACATCTTGTTGAGGGCAGGGGAGTA CTGTAGGAAGAGGAAGGAGACAGAGTTGAAAGTCAGGG	194
	CAACAAGATGTTTTGCC	195
	GGCAAACATCTTGTTG	196
In 1 pedigree consistent with the Li-Fraumeni syndrome, a germline G-to-T transversion at codon 272 (valine to leucine) was found.	TCTTGCTTCTCTTTTCTATCCTGAGTAGTGGTAATCTACTGG GACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGA GAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGA	197
	TCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAG GACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTA GATTACCACTACTCAGGATAGGAAAAGAGAAGCAAGA	198
	GCTTTGAGGTGCGTGTT	199
	AACACGCACCTCAAAGC	200
A ser241-to-phe mutation due to a TCC-to-TTC change was found in a patient with hepatoblastoma and multiple foci of osteosarcoma	TTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACAA CTACATGTGTAAACAGTTCCTGCATGGGCGGCATGAACCGGAG GCCCATCCTCACCATCATCACTGGAAGACTCCAG	201
	CTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCCG GTTTCATGCCGCCCATGCAGGAAGTGTACACATGTAGTTGTA GTGGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAA	202

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TAACAGTT <u>C</u> CTGCATGG	203
	CCATGCAG <u>G</u> AACTGTTA	204
An AAG-to-TAG change of codon 120, resulting in conversion from lysine to a stop codon, was found in a patient with osteosarcoma and adenocarcinoma of the lung at age 18 and brain tumor (glioma) at the age of 27.	CAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTC TTGCATTCTGGGACAGCC <u>A</u> AGTCTGTGACTTGCACGGTCAGT TGCCCTGAGGGGCTGGCTTCCATGAGACTTCAATGCC	205
	GGCATTGAAGTCTCATGGAAGCCAGCCCCTCAGGGCAACTG ACCGTGCAAGTCACAGACT <u>I</u> GGCTGTCCCAGAATGCAAGAAG CCCAGACGGAAACCGTAGCTGCCCTGGTAGGTTTTCTG	206
	GGACAGCC <u>A</u> AGTCTGTG	207
	CACAGACT <u>I</u> GGCTGTCC	208
A CGG-to-TGG change at codon 282, resulting in the substitution of tryptophan for arginine, was found in a patient who developed osteosarcoma at the age of 10 years.	GGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGT GCCTGTCCTGGGAGAGAC <u>C</u> GGCGCACAGAGGAAGAGAATCT CCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCCAG	209
	CTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGA TTCTCTTCCTCTGTGCGCC <u>G</u> TCTCTCCAGGACAGGCACAA ACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACC	210
	GGAGAGAC <u>C</u> GGCGCACA	211
	TGTGCGCC <u>G</u> TCTCTCC	212
In 5 of 6 anaplastic carcinomas of the thyroid and in an anaplastic carcinoma thyroid cell line ARO, a CGT-to-CAT mutation converted arginine-273 to histidine.	GCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACG GAACAGCTTTGAGGTG <u>C</u> GTGTTTGTGCCTGTCCTGGGAGAGA CCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGG	213
	CCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTC CCAGGACAGGCACAAAC <u>A</u> CGCACCTCAAAGCTGTTCCGTCCC AGTAGATTACCACTACTCAGGATAGGAAAAGAGAAGC	214
	TGAGGTG <u>C</u> GTGTTTGTG	215
	CACAAAC <u>A</u> CGCACCTCA	216

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
A germline GGA-to-GTA mutation resulting in a change of glycine-325 to valine was found in a patient who had non-Hodgkin lymphoma diagnosed at age 17 and colon carcinoma at age 26.	TCCTAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAA AGAAGAAACCACTGGATGGAGAATATTTACCCCTTCAGGTACT AAGTCTTGGGACCTCTTATCAAGTGGAAAGTTTCCA	217
	TGGAAACTTTCCACTTGATAAGAGGTCCCAAGACTTAGTACCT GAAGGGTGAAATATTCTCCATCCAGTGGTTTCTTCTTTGGCTG GGGAGAGGAGCTGGTGTGTTGGGCAGTGCTAGGA	218
	ACTGGATGGAGAATATT	219
	AATATTCTCCATCCAGT	220
CGC-CCC Arg-72 to Pro association with Lung cancer	AATGGTTCCTGAAGACCCAGGTCCAGATGAAGCTCCCAGAA TGCCAGAGGCTGCTCCCCGCGTGGCCCCCTGCACCAGCAGCT CCTACACCGGCGGCCCTGCACCAGCCCCCTCCTGGCC	221
	GGCCAGGAGGGGGCTGGTGCAGGGGCGCCGGTGTAGGAG CTGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATT CTGGGAGCTTCATCTGGACCTGGGTCTTCAGTGAACCATT	222
	TGCTCCCCGCGTGGCCC	223
	GGGCCACGCGGGGAGCA	224
CCG-CTG Pro-82 to Leu Breast cancer	AAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCCT GCACCAGCAGCTCCTACACCGGCGGCCCTGCACCAGCCCC CTCCTGGCCCCCTGTCATCTTCTGTCCCTTCCCAGAAAAC	225
	GTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGGAGGG GGCTGGTGCAGGGGCGCCGGTGTAGGAGCTGCTGGTGCA GGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTT	226
	TCCTACACCGGCGGCC	227
	GGGCCGCCGGTGTAGGA	228
cCAA-TAA Gln-136 to Term Li-Fraumeni syndrome	TTCAACTCTGTCTCCTTCCTCTTCTACAGTACTCCCCTGCCC TCAACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGC AGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCC	229
	GGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACA GGGCAGGTCTTGGCCAGTTGGCAAAACATCTTGTTGAGGGCA GGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTTGAA	230
	TGTTTTGCCAACTGGCC	231
	GGCCAGTTGGCAAAACA	232

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
TGC-TAC Cys-141 to Tyr Li-Fraumeni syndrome	TCCTCTTCCTACAGTACTCCCCTGCCCTCAACAAGATGTTTTG CCAAGTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTC CACACCCCCGCCCGGCACCCGCGTCCGCGCCATGGC	233
	GCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAAT CAACCCACAGCTGCACAGGGCAGGTCTTGCCAGTTGGCAA AACATCTTGTTGAGGGCAGGGGAGTACTGTAGGAAGAGGA	234
	CAAGACCTGCCCTGTGC	235
	GCACAGGGCAGGTCTTG	236
aCCC-TCC Pro-151 to Ser Li-Fraumeni syndrome	AACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAG CTGTGGGTTGATTCACACCCCCGCCCGGCACCCGCGTCCG CGCCATGGCCATCTACAAGCAGTCACAGCACATGACGG	237
	CCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGG ACGCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCT GCACAGGGCAGGTCTTGCCAGTTGGCAAACATCTTGTT	238
	ATTCCACACCCCCGCC	239
	GGCGGGGGTGTGGAAT	240
CCG-CTG Pro-152 to Leu Adrenocortical carcinoma	AGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGT GGGTTGATTCACACCCCCGCCCGGCACCCGCGTCCGCGCC ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGT	241
	ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCG CGGACGCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACA GCTGCACAGGGCAGGTCTTGCCAGTTGGCAAACATCT	242
	CACACCCCCGCCCGGCA	243
	TGCCGGGCGGGGGTGTG	244
GGC-GTC Gly-154 to Val Glioblastoma	TTTGCCAAGTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTG ATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATGGCC ATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAG	245
	CTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCC ATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAATCAA CCACAGCTGCACAGGGCAGGTCTTGCCAGTTGGCAA	246
	CCCGCCCGGCACCCGCG	247
	CGCGGGTGCCGGGCGGG	248
CGC-CAC Arg-175 to His Li-Fraumeni syndrome	CCCGCGTCCGCGCCATGGCCATCTACAAGCAGTCACAGCAC ATGACGGAGGTTGTGAGGCGCTGCCCCACCATGAGCGCTG CTCAGATAGCGATGGTGAGCAGCTGGGGCTGGAGAGACG	249

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CGTCTCTCCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAG CGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTG CTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGG	250
	TGTGAGGCGCTGCCCCC	251
	GGGGGCAGCGCCTCACA	252
tGAG-AAG Glu-180 to Lys Li-Fraumeni syndrome	ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTG AGGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCGATGG TGAGCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGC	253
	GCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCACCAT CGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACA ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCAT	254
	CCCACCATGAGCGCTGC	255
	GCAGCGCTCATGGTGGG	256
gCGC-TGC Arg-181 to Cys Breast cancer	GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGG CGCTGCCCCACCATGAGCGCTGCTCAGATAGCGATGGTGA GCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCA	257
	TGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCA CCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCT CACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGC	258
	ACCATGAGCGCTGCTCA	259
	TGAGCAGCGCTCATGGT	260
CGC-CAC Arg-81 to His Breast cancer	CCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGC GCTGCCCCACCATGAGCGCTGCTCAGATAGCGATGGTGA CAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCA	261
	CTGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTC ACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCC TCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGG	262
	CCATGAGCGCTGCTCAG	263
	CTGAGCAGCGCTCATGG	264
CAT-CGT His-193 to Arg Li-Fraumeni syndrome	CCAGGGTCCCCAGGCCTCTGATTCTCACTGATTGCTCTTAG GTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAATT TGCGTGTGGAGTATTGGATGACAGAAACACTTTTCG	265
	CGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTC CTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGA GCAATCAGTGAGGAATCAGAGGCCTGGGGACCCTGG	266

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TCCTCAGCATCTTATCC	267
	GGATAAGATGCTGAGGA	268
cCGA-TGA Arg-196 to Term Adrenocortical carcinoma	CCCAGGCCTCTGATTCTCACTGATTGCTCTTAGGTCTGGCC CCTCCTCAGCATCTTATCCGAGTGGAAGGAAATTTGCGTGTG GAGTATTTGGATGACAGAAACACTTTTCGACATAGTG	269
	CACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACG CAAATTTCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAG ACCTAAGAGCAATCAGTGAGGAATCAGAGGCCTGGG	270
	ATCTTATCCGAGTGGA	271
	TTCCACTCGGATAAGAT	272
cAGA-TGA Arg-209 to Term Li-Fraumeni syndrome	GCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAATTTGCGT GTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTG GTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGCAA	273
	TTGCAAACCAGACCTCAGGCGGCTCATAGGGCACCACCACA CTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCA AATTTCTTCCACTCGGATAAGATGCTGAGGAGGGGC	274
	TGGATGACAGAAACACT	275
	AGTGTTTCTGTCATCCA	276
tCGA-TGA Arg-213 to Term Li-Fraumeni syndrome	CATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTG GATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT GAGCCGCCTGAGGTCTGGTTTGCAACTGGGGTCTCTG	277
	CAGAGACCCAGTTGCAAACCAGACCTCAGGCGGCTCATAG GGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAAT ACTCCACACGCAAATTTCTTCCACTCGGATAAGATG	278
	ACACTTTTCGACATAGT	279
	ACTATGTCGAAAAGTGT	280
gCCC-TCC Pro-219 to Ser Adrenocortical carcinoma	GGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTC GACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGG TTTGCAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGT	281
	ACCCTTAACCCCTCCTCCCAGAGACCCAGTTGCAAACCAGA CCTCAGGCGGCTCATAGGGCACCACCACACTATGTCGAAAAG TGTTTCTGTCATCCAAATACTCCACACGCAAATTTCC	282
	TGGTGGTGCCCTATGAG	283
	CTCATAGGGCACCACCA	284

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
TAT-TGT Tyr-220 to Cys Li-Fraumeni syndrome	ATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACA TAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTG CAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGTGGTT	285
	AACCACCCTTAACCCCTCCTCCCAGAGACCCAGTTGCAAAC CAGACCTCAGGCGGCTCATAGGGCACCACCACACTATGTCG AAAAGTGTTTCTGTCTATCCAAATACTCCACACGCAAAT	286
	GGTGCCCTATGAGCCGC	287
	GCGGCTCATAGGGCACC	288
cTCT-ACT Ser-227 to Thr Rhabdomyosarcoma	CACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTGGGCCTG TGTTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTAC AACTACATGTGTAAACAGTTCCTGCATGGGCGGCATGA	289
	TCATGCCGCCCATGCAGGAAGTGTACACATGTAGTTGTAGT GGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAACACAG GCCCAAGATGAGGCCAGTGCGCCTTGGGGAGACCTGTG	290
	AGGTTGGCTCTGACTGT	291
	ACAGTCAGAGCCAACCT	292
cCAC-AAC His-233 to Asn Glioma	GCACTGGCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGC TCTGACTGTACCACCATCCACTACAACATCATGTGTAACAGTT CCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCA	293
	TGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAAGTGT TTACACATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCA ACCTAGGAGATAACACAGGCCCAAGATGAGGCCAGTGC	294
	CCACCATCCACTACAAC	295
	GTTGTAGTGGATGGTGG	296
cAAC-GAC Asn-235 to Asp Adrenocortical carcinoma	GCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGAC TGTAACCATCCACTACAACATCATGTGTAACAGTTCCTGCA TGGGCGGCATGAACCGGAGGCCCATCCTCACCATCA	297
	TGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAG GAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTCA GAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGGC	298
	TCCACTACAACATCATG	299
	CATGTAGTTGTAGTGGA	300
AAC-AGC Asn-235 to Ser Rhabdomyosarcoma	CCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGACT GTACCACCATCCACTACAACATCATGTGTAACAGTTCCTGCAT GGGCGGCATGAACCGGAGGCCCATCCTCACCATCAT	301

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ATGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCA GGAAGTGTACACATGTAGTTGTAGTGGATGGTGGTACAGTC AGAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGG	302
	CCACTACA <u>A</u> CTACATGT	303
	ACATGTAGTTGTAGTGG	304
ATCc-ATG Ile-251 to Met Glioma	CATCCACTACA <u>A</u> CTACATGTGTAAACAGTTCCTGCATGGGCGG CATGAACCGGAGGCCCAT <u>C</u> CTCACCATCATCACACTGGAAGA CTCCAGGTCAGGAGCCACTTGCCACCCTGCACACTGG	305
	CCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTT CCAGTGTGATGATGGTGA <u>G</u> ATGGGCCTCCGGTTCATGCCG CCCATGCAGGA <u>A</u> CTGTTACACATGTAGTTGTAGTGGATG	306
	AGGCCCAT <u>C</u> CTCACCAT	307
	ATGGTGAGGATGGGCCT	308
ACA-ATA Thr-256 to Ile Glioblastoma	ACATGTGTAAACAGTTCCTGCATGGGCGGCATGAACCGGAGG CCCATCCTCACCATCATCA <u>C</u> ACTGGAAGACTCCAGGTCAGGA GCCACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCA	309
	TGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGGCTCC TGACCTGGAGTCTTCCAGT <u>G</u> TGATGATGGTGAAGGATGGGCCT CCGGTTCATGCCGCCCATGCAGGA <u>A</u> CTGTTACACATGT	310
	CATCATCA <u>C</u> ACTGGAAG	311
	CTTCCAGT <u>G</u> TGATGATG	312
CTG-CAG Leu-257 to Gln Li-Fraumeni syndrome	TGTGTAAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCC ATCCTCACCATCATCACACT <u>G</u> GGAAGACTCCAGGTCAGGAGCC ACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCC	313
	GGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGG CTCCTGACCTGGAGTCTTCC <u>A</u> GTGTGATGATGGTGAAGGATGG GCCTCCGGTTCATGCCGCCCATGCAGGA <u>A</u> CTGTTACACA	314
	CATCACACT <u>G</u> GGAAGACT	315
	AGTCTTCC <u>A</u> GTGTGATG	316
CTG-CCG Leu-265 to Pro Li-Fraumeni syndrome	GACCTGATTTCTTACTGCCTCTTGCTTCTTTTTCTATCCT GAGTAGTGGTAATCTACT <u>G</u> GGACGGAACAGCTTTGAGGTGCG TGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGA	317
	TCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCAC CTCAAAGCTGTTCCGTCCC <u>A</u> GTAGATTACCACTACTCAGGAT AGGAAAAGAGAAGCAAGAGGCAGTAAGGAAATCAGGTC	318

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATCTACTGGGACGGA	319
	TCCGTCCCAGTAGATTA	320
gCGT-TGT Arg-273 to Cys Li-Fraumeni syndrome	TGCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGAC GGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAG	321
	CTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCC CAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCA GTAGATTACCACTACTCAGGATAGGAAAAGAGAAGCA	322
	TTGAGGTGCGTGTTTGT	323
	ACAAACACGCACCTCAA	324
TGT-TAT Cys-275 to Tyr Li-Fraumeni syndrome	CTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACA GCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGAGACCGG CGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCC	325
	GGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGG TCTCTCCAGGACAGGCACAACACGCACCTCAAAGCTGTTT CGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAG	326
	GCGTGTTTGTGCCTGTC	327
	GACAGGCACAACACGC	328
CCT-CTT Pro-278 to Leu Breast cancer	TCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGG TGCGTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAG GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGA	329
	TCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCT GTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTC AAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGA	330
	TGCCTGTCCTGGGAGAG	331
	CTCTCCCAGGACAGGCA	332
AGA-AAA Arg-280 to Lys Glioma	GTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTG TTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAG AATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCC	333
	GGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCT TCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACG CACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTAC	334
	TCCTGGGAGAGACCGGC	335
	GCCGGTCTCTCCCAGGA	336

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
GAA-GCA Glu-286 to Ala Adrenocortical carcinoma	GGAACAGCTTTGAGGTGCGTGTGTTGTGCCTGTCCTGGGAGA GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGA GCCTCACCACGAGCTGCCCCAGGGAGCACTAAGCGAGG	337
	CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTC CCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCT CCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCC	338
	AGAGGAAGAGAATCTCC	339
	GGAGATTCTCTTCCTCT	340
CGA-CCA Arg-306 to Pro Rhabdomyosarcoma	AAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTG CCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAGA AGCGGTGGAGGAGACCAAGGGTGCAGTTATGCCTCAGAT	341
	ATCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCT TGTCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGC TCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTT	342
	CACTAAGCGAGGTAAGC	343
	GCTTACCTCGCTTAGTG	344
gCGA-TGA Arg-306 to Term Li-Fraumeni syndrome	GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCT GCCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAG AAGCGGTGGAGGAGACCAAGGGTGCAGTTATGCCTCAGA	345
	TCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTT GTCCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGCT CGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTC	346
	GCACTAAGCGAGGTAAG	347
	CTTACCTCGCTTAGTGC	348
gCGC-TGC Arg-337 to Cys Osteosarcoma	GGTACTGTGAATATACTTACTTCTCCCCCTCCTCTGTTGCTGC AGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTG AATGAGGCCTTGGAAGTCAAGGATGCCAGGCTGGGA	349
	TCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTGAGCT CTCGGAACATCTCGAAGCGCTCACGCCACGGATCTGCAGC AACAGAGGAGGGGGAGAAGTAAGTATATTCACAGTACC	350
	GGCGTGAGCGCTTCGAG	351
	CTCGAAGCGCTCACGCC	352
CTG-CCG Leu-344 to Pro Li-Fraumeni syndrome	CTCCCCCTCCTCTGTTGCTGCAGATCCGTGGGCGTGAGCGC TTCGAGATGTTCCGAGAGCTGAATGAGGCCTTGGAAGTCAAG GATGCCAGGCTGGGAAGGAGCCAGGGGGGAGCAGGGC	353

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCCTGCTCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTT GAGTTCCAAGGCCTCATT <u>C</u> AGCTCTCGGAACATCTCGAAGCG CTCACGCCACGGATCTGCAGCAACAGAGGAGGGGGAG	354
	CCGAGAGCT <u>T</u> GAATGAGG	355
	CCTCATT <u>C</u> AGCTCTCGG	356

EXAMPLE 6

beta globin

Hemoglobin, the major protein in the red blood cell, binds oxygen reversibly and is responsible for the cells' capacity to transport oxygen to the tissues. In adults, the major hemoglobin is hemoglobin A, a tetrameric protein consisting of two identical alpha globin chains and two beta globin chains. Disorders involving hemoglobin are among the most common genetic disorders worldwide, with approximately 5% of the world's population being carriers for clinically important hemoglobin mutations. Approximately 300,000 severely affected homozygotes or compound heterozygotes are born each year.

Mutation of the glutamic acid at position 7 in beta globin to valine causes sickle cell anemia, the clinical manifestations of which are well known. Mutations that cause absence of beta chain cause beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. For clinical purposes, beta-thalassemia is divided into thalassemia major (transfusion dependent), thalassemia intermedia (of intermediate severity), and thalassemia minor (asymptomatic). Patients with thalassemia major present in the first year of life with severe anemia; they are unable to maintain a hemoglobin level about 5 gm/dl.

The beta-thalassemias were among the first human genetic diseases to be examined by means of recombinant DNA analysis. Baysal et al., *Hemoglobin* 19(3-4):213-36 (1995) and others provide a compendium of mutations that result in beta-thalassemia.

Hemoglobin disorders were among the first to be considered for gene therapy. Transcriptional silencing of genes transferred into hematopoietic stem cells, however, poses one of the most significant challenges to its success. If the transferred gene is not completely silenced, a progressive decline in gene expression is often observed. Position effect variegation (PEV) and silencing mechanisms may act on a transferred globin gene residing in chromatin outside of the normal globin locus during the important terminal phases of erythroblast development when globin transcripts normally

accumulate rapidly despite heterochromatization and shutdown of the rest of the genome. The attached table discloses the correcting oligonucleotide base sequences for the beta globin oligonucleotides of the invention.

Table 12
Beta Globin Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Sickle Cell Anemia GLU-7-VAL GAG to GTG	TCTGACACAACCTGTGTTCACTAGCAACCTCAAACAGACACCA TGGTGACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCC CTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA	357
	TCACCACCAACTTCATCCACGTTACCTTGCCCCACAGGGCA GTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGGT GTCTGTTTGAGGTTGCTAGTGAACACAGTTGTGTCAGA	358
	GACTCCTGAGGAGAAGT	359
	ACTTCTCCTCAGGAGTC	360
Thalassaemia Beta MET-0-ARG ATG to AGG	CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCAATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	361
	ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	362
	AGACACCATGGTGCACC	363
	GGTGCACCATGGTGTCT	364
Thalassaemia Beta MET-0-ILE ATG to ATA	TATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAA CCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	365
	CACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGC TAGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATA	366
	GACACCATGGTGCACCT	367
	AGGTGCACCATGGTGTCT	368
Thalassaemia Beta MET-0-ILE ATG to ATT	TATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAA CCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	369

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGC TAGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATA	370
	GACACCATGGTGCACCT	371
	AGGTGCACCATGGTGTCT	372
Thalassaemia Beta MET-0-LYS ATG to AAG	CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	373
	ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	374
	AGACACCATGGTGCACC	375
	GGTGCACCATGGTGTCT	376
Thalassaemia Beta MET-0-THR ATG to ACG	CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	377
	ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	378
	AGACACCATGGTGCACC	379
	GGTGCACCATGGTGTCT	380
Thalassaemia Beta MET-0-VAL ATG to GTG	TCTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGC AACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAG AAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACG	381
	CGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCC TCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTAG TGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	382
	CAGACACCATGGTGCAC	383
	GTGCACCATGGTGTCTG	384
Thalassaemia Beta TRP-16-Term TGG to TGA	TCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGT CTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAA GTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTA	385
	TAACCTTGATACCAACCTGCCAGGGCCTCACCACCAACTTC ATCCACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACT TCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGA	386

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCCTGTGGGGCAAGGT	387
	ACCTTGCCCCACAGGGC	388
Thalassaemia Beta TRP-16-Term TGG to TAG	CTCAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAG TCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGA AGTTGGTGGTGAAGGCCCTGGGCAGGTTGGTATCAAGGTT	389
	AACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTCA TCCACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTT CTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAG	390
	TGCCCTGTGGGGCAAGG	391
	CCTTGCCCCACAGGGCA	392
Thalassaemia Beta LYS-18-Term AAG to TAG	ACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGTCTGC CGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTG GTGGTGAAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAG	393
	CTTGTAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAA CTTCATCCACGTTACCTTGCCCCACAGGGCAGTAACGGCA GACTTCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGT	394
	TGTGGGGCAAGGTGAAC	395
	GTTACCTTGCCCCACA	396
Thalassaemia Beta ASN-20-SER AAC to AGC	CCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACT GCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA GGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTT	397
	AACCTGTCTTGTAACCTTGATACCAACCTGCCCAGGGCCTCA CCACCAACTTCATCCACGTTACCTTGCCCCACAGGGCAGTA ACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGG	398
	CAAGGTGAACGTGGATG	399
	CATCCACGTTACCTTG	400
Thalassaemia Beta GLU-23-ALA GAA to GCA	ACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGG GGCAAGGTGAACGTGGATGAAGTTGGTGGTGAAGGCCCTGG GCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGAC	401
	GTCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCC AGGGCCTCACCACCAACTTCATCCACGTTACCTTGCCCCAC AGGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGT	402
	CGTGGATGAAGTTGGTG	403
	CACCAACTTCATCCACG	404

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta GLU-23-term GAA to TAA	CACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTG GGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTG GGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGA	405
	TCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCA GGGCCTCACCACCAACTTCATCCACGTTACCTTGCCCCACA GGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTG	406
	ACGTGGATGAAGTTGGT	407
	ACCAACTTCATCCACGT	408
Thalassaemia Beta GLU-27-LYS GAG to AAG	GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACT	409
	AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGTTCA CTTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC	410
	TTGGTGGTGAGGCCCTG	411
	CAGGGCCTCACCACCAA	412
Thalassaemia Beta GLU-27-Term GAG to TAG	GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACT	413
	AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGTTCA CTTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC	414
	TTGGTGGTGAGGCCCTG	415
	CAGGGCCTCACCACCAA	416
Thalassaemia Beta ALA-28-SER GCC to TCC	GAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAACGT GGATGCAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAA GGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACTGGG	417
	CCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGA TACCAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGT TCACTTTGCCCCACAGGGCATTGACAGCAGTCTTCTC	418
	GTGGTGAGGCCCTGGGC	419
	GCCCAGGGCCTCACCAC	420

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta ARG-31-THR AGG to ACG	CTGTCAATGCCCTGTGGGGCAAAGTGAACGTGGATGCAGTT GGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTATAAGA GAGGCTCAAGGAGGCCAATGGAACTGGGCATGTGTAGA	421
	TCTACACATGCCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTT ATAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTG CATCCACGTTCACTTTGCCCCACAGGGCATTGACAG	422
	CCTGGGCAGGTTGGTAT	423
	ATACCAACCTGCCCAGG	424
Thalassaemia Beta Leu-33-GLN CTG to CAG	TGGGTTTCTGATAGGCACTGACTCTCTGTCCCTTGGGCTGTT TTCCTACCCTCAGATTACTGGTGGTCTACCCTTGGACCCAGA GGTTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGA	425
	TCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAACCTCTG GGTCCAAGGGTAGACCACCAGTAATCTGAGGGTAGGAAAAC AGCCCAAGGGACAGAGAGTCAGTGCCTATCAGAAACCCA	426
	CAGATTACTGGTGGTCT	427
	AGACCACCAGTAATCTG	428
Thalassaemia Beta TYR-36-Term TAC to TAA	ATAGGCACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCT CAGATTACTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGA GTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTATG	429
	CATAACAGCATCAGGAGAGGACAGATCCCCAAAGGACTCAA GAACCTCTGGGTCCAAGGGTAGACCACCAGTAATCTGAGGG TAGGAAAACAGCCCAAGGGACAGAGAGTCAGTGCCTAT	430
	GTGGTCTACCCTTGGAC	431
	GTCCAAGGGTAGACCAC	432
Thalassaemia Beta TRP-38-Term TGG to TGA	ACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGATT ACTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTT TGGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAAC	433
	GTTGCCCATACAGCATCAGGAGAGGACAGATCCCCAAAGG ACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGTAATC TGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCAGT	434
	TACCCTTGGACCCAGAG	435
	CTCTGGGTCCAAGGGTA	436
Thalassaemia Beta TRP-38-Term TGG to TAG	CACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGAT TACTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCT TTGGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAA	437

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCAAAGGA CTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGTAATCT GAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCAGTG	438
	CTACCCTTGACCCAGA	439
	TCTGGGTCCAAGGGTAG	440
Thalassaemia Beta GLN-40-Term CAG-TAG	ACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGATTACTG GTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGG GATCTGTCCTCTCCTGATGCTGTTATGGGCAACCCTA	441
	TAGGGTTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCA AAGGACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAG TAATCTGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGT	442
	CTTGGACCCAGAGGTTCT	443
	GAACCTCTGGGTCCAAG	444
Thalassaemia Beta GLU-44-Term GAG to TAG	TTGGGCTGTTTTCTACCCTCAGATTACTGGTGGTCTACCCT TGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTGTCCTCT CCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTC	445
	GAGCCTTCACCTTAGGGTTGCCCAT AACAGCATCAGGAGAG GACAGATCCCCAAAGGACTCAAAGAACCTCTGGGTCCAAGG GTAGACCACCAGTAATCTGAGGGTAGGAAAACAGCCCAA	446
	GGTTCTTTGAGTCCTTT	447
	AAAGGACTCAAAGAACC	448
Thalassaemia Beta LYS-62-Term AAG to TAG	TTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTA TGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTGCTA GGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACC	449
	GGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGC ACCTTCTTGCCATGAGCCTTCACCTTAGGGTTGCCATAACA GCATCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAA	450
	CTAAGGTGAAGGCTCAT	451
	ATGAGCCTTCACCTTAG	452
Thalassaemia Beta SER-73-ARG AGT to AGA	TGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGA AGGTGCTAGGTGCCTTTAGTGATGGCCTGGCTCACCTGGAC AACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTGCAC	453
	GTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTC CAGGTGAGCCAGGCCATCACTAAAGGCACCTAGCACCTTCT TGCCATGAGCCTTCACCTTAGGGTTGCCCAT AACAGCA	454

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCTTTAGT <u>G</u> ATGGCCT	455
	AGGCCATCACTAAAGGC	456
Haemolytic Anaemia GLY-75-VAL GGC to GTC	TTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTG CTAGGTGCCTTTAGT <u>G</u> ATGGCCTGGCTCACCTGGACAACCT CAAGGGCACTTTTTCTCAGCTGAGTGAGCTGCACTGTGA	457
	TCACAGTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAG GTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGCA CCTTCTTGCCATGAGCCTTCACCTTAGGGTTGCCATAA	458
	TAGTGATGGCCTGGCTC	459
	GAGCCAGGCCATCACTA	460
Thalassaemia Beta GLU-91-Term GAG to TAG	GCCTTTAGT <u>G</u> ATGGCCTGGCTCACCTGGACAACCTCAAGGG CACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGC ACGTGGATCCTGAGAACTTCAGGGTGAGTCTATGGGACC	461
	GGTCCCATAGACTCACCTGAAGTTCTCAGGATCCACGTGCA GCTTGTACAGTGCAGCTCACTCAGTGTGGCAAAGGTGCCC TTGAGGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGC	462
	CACTGAGTGAGCTGCAC	463
	GTGCAGCTCACTCAGTG	464
Thalassaemia Beta VAL-99-MET GTG to ATG	CTGGACAACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTG CACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGGT GAGTCCAGGAGATGCTTCACTTTTCTCTTTTACTTTC	465
	GAAAGTAAAAAGAGAAAAGTGAAGCATCTCCTGGACTCACCC TGAAGTTCTCAGGATCCACGTGCAGCTTGTACAGTGCAGCT CACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTCCAG	466
	AGCTGCACGTGGATCCT	467
	AGGATCCACGTGCAGCT	468
Thalassaemia Beta LEU-111-PRO CTG-CCG	CCCTTTTGCTAATCATGTTACATACCTCTTATCTTCCTCCCACA GCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACT TTGGCAAAGAATTCACCCACCAGTGCAGGCTGCCTA	469
	TAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCCAAAGTG ATGGGCCAGCACACAGACCAGCACGTTGCCAGGAGCTGTG GGAGGAAGATAAGAGGTATGAACATGATTAGCAAAGGG	470
	CAACGTGCTGGTCTGTG	471
	CACAGACCAGCACGTTG	472

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta CYS-113-Term TGT to TGA	GCTAATCATGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTG GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAA	473
	TTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCC AAAGTGATGGGCCAGCACACAGACCAGCACGTTGCCAGGA GCTGTGGGAGGAAGATAAGAGGTATGAACATGATTAGC	474
	CTGGTCTGTGTGCTGGC	475
	GCCAGCACACAGACCAG	476
Thalassaemia Beta LEU-115-PRO CTG to CCG	TCATGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCA ACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAAT TCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGT	477
	ACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCT TTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC CAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACATGA	478
	CTGTGTGCTGGCCCATC	479
	GATGGGCCAGCACACAG	480
Thalassaemia Beta ALA-116-ASP GCC to GAC	TGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACG TGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCA CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGC	481
	GCCACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAA TTCTTTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTT GCCAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACA	482
	TGTGCTGGCCCATCACT	483
	AGTGATGGGCCAGCACA	484
Thalassaemia Beta GLU-122-Term GAA to TAA	TTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCT GGCCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCAGG CTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCC	485
	GGGCATTAGCCACACCAGCCACCACTTTCTGATAGGCAGCC TGCACTGGTGGGGTGAATTCTTTGCCAAAGTGATGGGCCAG CACACAGACCAGCACGTTGCCAGGAGCTGTGGGAGGAA	486
	TTGGCAAAGAATTCACC	487
	GGTGAATTCTTTGCCAA	488
Thalassaemia Beta GLN-128-PRO CAG to CCG	GCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA GAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACTA	489

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCAC CACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTT GCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGC	490
	ACCAGTGCAGGCTGCCT	491
	AGGCAGCCTGCACTGGT	492
Thalassaemia Beta GLN-128-Term CAG to TAG	GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCACCAAGTGCAAGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACT	493
	AGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCACC ACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTG CCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC	494
	CACCAGTGCAGGCTGCC	495
	GGCAGCCTGCACTGGTG	496
Thalassaemia Beta GLN-132-LYS CAG to AAG	GTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCA CCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGC TAATGCCCTGGCCACAAGTATCACTAAGCTCGCTTTC	497
	GAAAGCGAGCTTAGTGATACTTGTGGGCCAGGGCATTAGCC ACACCAGCCACCACTTTCTGATAGGCAGCCTGCACTGGTGG GGTGAATTCTTTGCCAAAGTGATGGGCCAGCACACAGAC	498
	CTGCCTATCAGAAAGTG	499
	CACTTTCTGATAGGCAG	500

EXAMPLE 7

Retinoblastoma

Retinoblastoma (RB) is an embryonic neoplasm of retinal origin. It almost always presents in early childhood and is often bilateral. The risk of osteogenic sarcoma is increased 500-fold in bilateral retinoblastoma patients, the bone malignancy being at sites removed from those exposed to radiation treatment of the eye tumor.

The retinoblastoma susceptibility gene (pRB; pRb) plays a pivotal role in the regulation of the cell cycle. pRB restrains cell cycle progression by maintaining a checkpoint in late G₁ that controls commitment of cells to enter S phase. The critical role that pRB plays in cell cycle regulation explains its

status as archetypal tumor suppressor: loss of pRB function results in an inability to maintain control of the G₁ checkpoint; unchecked progression through the cell cycle is, in turn, a hallmark of neoplasia.

Blanquet et al., *Hum. Molec. Genet.* 4: 383-388 (1995) performed a mutation survey of the RB1 gene in 232 patients with hereditary or nonhereditary retinoblastoma. They systematically explored all 27 exons and flanking sequences, as well as the promoter. All types of point mutations were represented and found to be unequally distributed along the RB1 gene sequence. In the population studied, exons 3, 8, 18, and 19 were preferentially altered. The attached table discloses the correcting oligonucleotide base sequences for the retinoblastoma oligonucleotides of the invention.

Table 13
pRB Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Trp99Term TGG-TAG	AATATTTGATCTTTATTTTTGTTCCCAGGGAGGTTATATTCAA AAGAAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCA GTTGACCTAGATGAGATGTCGTTCACTTTTACTGA	501
	TCAGTAAAAGTGAACGACATCTCATCTAGGTCAACTGCTGCA ATAAAGATACAGATTCCCCACAGTTCCTTTTTCTTTGAATATA ACCTCCCTGGGAACAAAAATAAAGATCAAATATT	502
	GGAAGTGTGGGGAATCT	503
	AGATCCCCACAGTTCC	504
Retinoblastoma Glu137Asp GAA-GAT	ATTACTTTTTCTATTCTTTCCTTTGTAGTGTCCATAAATTCTT TAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAAT GCTATGTCAAGACTGTTGAAGAAGTATGATGTA	505
	TACATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACTT TGGTACTGGTATCAATTCTTTTAGTAAGTTAAAGAATTTATGG ACACTACAAAGGAAAGAATAGAAAAAGTAAAT	506
	CTAAAAGAAATTGATAC	507
	GTATCAATTTCTTTTAG	508
Retinoblastoma Glu137Term GAA-TAA	TGATTTACTTTTTCTATTCTTTCCTTTGTAGTGTCCATAAATT CTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGAT AATGCTATGTCAAGACTGTTGAAGAAGTATGATG	509

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACTTT GGTACTGGTATCAATTTCTTTTAGTAAGTTAAAGAATTTATGG ACACTACAAAGGAAAGAATAGAAAAAGTAAATCA	510
	TACTAAAAGAAATTGAT	511
	ATCAATTTCTTTTAGTA	512
Retinoblastoma Gln176Term CAA-TAA	AAAATGTTAAAAAGTCATAATGTTTTCTTTTCAGGACATGTGA ACTTATATATTTGACACAACCCAGCAGTTCGTAAGTAGTTCAC AGAATGTTATTTTCACTTAAAAAAAAGATTTT	513
	AAAATCTTTTTTTTAAAGTGAAAAATAACATTCTGTGAACTACT TACGAACTGCTGGGTTGTGTCAAATATATAAGTTCACATGTCC TGAAAAGAAAAACATTATGACTTTTAAACATTTT	514
	ATTTGACACAACCCAGC	515
	GCTGGGTTGTGTCAAAT	516
Retinoblastoma Ile185Thr ATA-ACA	TGATACATTTTCTGTTTTTTTCTGCTTTCTATTTGTTTAATA GGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTC TTGGATCACATTTTATTAGCTAAAGGTAAGTT	517
	AACTTACCTTTAGCTAATAAAAATGTGATCCAAGAACTTTTA GCACCAATGCAGAATTTATTTTCAGTAGATATCCTATTAAACAA ATAGAAAGCAGAAAAAAACAGGAAAAATGTATCA	518
	TACTGAAATAAATTCTG	519
	CAGAATTTATTTTCAGTA	520
Retinoblastoma Gln207Term CAA-TAA	AAAGATCTGAATCTCTAACTTTCTTTAAAAATGTACATTTTTT TTCAGGGGAAGTATTACAATGGAAGATGATCTGGTGATTTC ATTTTCAGTTAATGCTATGTGTCCTTGACTATTTTA	521
	TAAATAGTCAAGGACACATAGCATTAACTGAAATGAAATCAC CAGATCATCTTCCATTTGTAATACTTCCCCTGAAAAAAAATG TACATTTTTAAAGAAAGTTAGAGATTCAGATCTTT	522
	AAGTATTACAAATGGAA	523
	TTCCATTTGTAATACTT	524
Retinoblastoma Arg251Term CGA to TGA	GTTCTTATCTAATTTACCACTTTTACAGAAACAGCTGTTATACC CATTAAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACA GGAGTGACGGATAGCAAAACAAGTAGAAAATGATA	525
	TATCATTTTCTAGTTGTTTTGCTATCCGTGCACTCCTGTTCTG ACCTCGCCTGGGTGTTGAGGTGAACCATTAATGGGTATAAC AGCTGTTTCTGTAAAGTGGTAAATTAGATAAGAAC	526

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTTCACCTCGAACACCC	527
	GGGTGTTGAGGTGAAC	28
Retinoblastoma Arg255Term CGA to TGA	TTTACCACTTTTACAGAAACAGCTGTTATACCCATTAATGGTT CACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACG GATAGCAAAACAACCTAGAAAATGATACAAGAATTATTG	529
	CAATAATTCTTGTATCATTTTCTAGTTGTTTTGCTATCCGTGCA CTCCTGTTCTGACCTCGCCTGGGTGTTGAGGTGAACCATTA ATGGGTATAACAGCTGTTTCTGTAAAAGTGGTAAA	530
	CACCCAGGCGAGGTCAG	531
	CTGACCTCGCCTGGGTG	532
Retinoblastoma Gln266Term CAA to TAA	ATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAG GAGTGCACGGATAGCAAAACAACCTAGAAAATGATACAAGAAT TATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAG	533
	CTATATTACATTCATGTTCTTTACAGAGAACTTCAATAATTCTT GTATCATTTTCTAGTTGTTTTGCTATCCGTGCACTCCTGTTCT GACCTCGCCTGGGTGTTGAGGTGAACCATTAAT	534
	TAGCAAAACAACCTAGAA	535
	TTCTAGTTGTTTTGCTA	536
Retinoblastoma Arg320Term CGA to TGA	TGACATGTAAAGGATAATTGTCAGTGACTTTTTCTTTCAAGG TTGAAAATCTTTCTAAAGGATACGAAGAAATTTATCTTAAAAAT AAAGATCTAGATGCAAGATTATTTTGGATCATG	537
	CATGATCCAAAAATAATCTTGCATCTAGATCTTTATTTTAAGA TAAATTTCTTCGTATCGTTTAGAAAGATTTTCAACCTTGAAAGA AAAAAGTCACTGACAATTATCCTTTACATGTCA	538
	TTTCTAAACGATACGAA	539
	TTCGTATCGTTTAGAAA	540
Retinoblastoma Gln354Term CAG to TAG	ACAAATTGTAAATTTTCAGTATGTGAATGACTTCACTTATTGTT ATTTAGTTTTGAAACAAGAGAACACCACGAAAAAGTAACCTT GATGAAGAGGTGAATGTAATTCCTCCACACACTC	541
	GAGTGTGTGGAGGAATTACATTCACCTCTTCATCAAGGTTAC TTTTTCGTGGTGTCTCTGTGTTTCAAACTAAATAACAATAA GTGAAGTCATTACATACTGAAAATTTACAATTTGT	542
	TTGAAACAAGAGACA	543
	TGTTCTCTGTGTTTCAA	544

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Arg358Gly CGA to GGA	TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGA AACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGT GAATGTAATTCCTCCACACACTCCAGTTAGGTATG	545
	CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTT CATCAAGGTTACTTTTTCTGGTGTCTCTGTGTTTCAAACCT AAATAACAATAAGTGAAGTCATTCACATACTGAAAA	546
	GAACACCACGAAAAAGT	547
	ACTTTTTCTGGTGTTC	548
Retinoblastoma Arg358Term CGA to TGA	TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGA AACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGT GAATGTAATTCCTCCACACACTCCAGTTAGGTATG	549
	CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTT CATCAAGGTTACTTTTTCTGGTGTCTCTGTGTTTCAAACCT AAATAACAATAAGTGAAGTCATTCACATACTGAAAA	550
	GAACACCACGAAAAAGT	551
	ACTTTTTCTGGTGTTC	552
Retinoblastoma Ser397Term TCA to TAA	CTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA GCAAGTGATCAACCTTCAGAAAATCTGATTTCTATTTTAACG TAAGCCATATATGAAACATTATTTATTGTAATAT	553
	ATATTACAATAAATAATGTTTCATATATGGCTTACGTTAAATA GGAAATCAGATTTTCTGAAGGTTGATCACTTGCTGAATTTAAA ATCATCATTAAATTGTTGGATAGTGTTACATAACAG	554
	TCAACCTTCAGAAAATC	555
	GATTTTCTGAAGGTTGA	556
Retinoblastoma Arg445Term CGA to TGA	TTTCATAATTGTGATTTTCTAAAATAGCAGGCTCTTATTTTCT TTTTGTTTGTGTAGCGATACAACTTGGAGTTGCTTGTAT TACCGAGTAATGGAATCCATGCTTAAATCAGTAA	557
	TACTGATTTAAGCATGGATTCCATTACTCGGTAATACAAGCG AACTCCAAGTTTGTATCGCTACAAACAAACAAAAGAAAAATA AGAGCCTGCTATTTTAGAAAATCACAATTATGAAA	558
	GTTTGTAGCGATACAAA	559
	TTTGTATCGCTACAAAC	560
Retinoblastoma Arg455Term CGA to TGA	GCTCTTATTTTCTTTTGTGTTTGTAGCGATACAACTTGG AGTTGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCA GTAAGTTAAAACAATATAAAAAATTCAGCCG	561

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGGCTGAAATTTTTTATATTGTTTTAACTTACTGATTTAAGC ATGGATTCCATTACTCGGTAATACAAGCGAACTCCAAGTTTGT ATCGCTACAAACAAACAAAAGAAAAATAAGAGC	562
	TGTATTACCGAGTAATG	563
	CATTACTCGGTAATACA	564
Retinoblastoma Arg552Term CGA to TGA	ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAA ATGATAAAACATTTAGAACGATGTGAACATCGAATCATGGAAT CCCTTGCATGGCTCTCAGTAAGTAGCTAAATAATTG	565
	CAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGATTCCAT GATTGATGTTACATCGTTCTAAATGTTTTATCATTCTCTTG TCAAGTTGCCTTCTGCTTTGATAAACTTTTCGAT	566
	ATTAGAACGATGTGAA	567
	TTCACATCGTTCTAAAT	568
Retinoblastoma Cys553Term TGT to TGA	AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTG CATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAA	569
	TTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGAT TCCATGATTGATGTTACATCGTTCTAAATGTTTTATCATTTT TCTTGTCAAGTTGCCTTCTGCTTTGATAAACTT	570
	GAACGATGTGAACATCG	571
	CGATGTTACATCGTTC	572
Retinoblastoma Glu554Term GAA to TAA	AGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAA AACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTG CATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAAA	573
	TTTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGA TTCCATGATTGATGTTACATCGTTCTAAATGTTTTATCATTT CTTTGTCAAGTTGCCTTCTGCTTTGATAAACT	574
	AACGATGTGAACATCGA	575
	TCGATGTTACATCGTT	576
Retinoblastoma Ser567Leu TCA to TTA	TACCTGGGAAAATTATGCTTACTAATGTGGTTTTAATTCATC ATGTTTCATATAGGATTACCTTTATTTGATCTTATTAACAAT CAAAGGACCGAGAAGGACCAACTGATCACCTTGA	577
	TCAAGGTGATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAA TAAGATCAAATAAAGGTGAATCCTATATGAAACATGATGAAAT TAAACCACATTAGTAAGCATAATTTCCAGGTA	578

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ATAGGATT <u>C</u> ACCTTTAT	579
	ATAAAGGTGAATCCTAT	580
Retinoblastoma Gln575Term CAA to TAA	AATGTGGTTTTAATTTATCATGTTTCATATAGGATTACCTTT ATTTGATCTTATTAA <u>C</u> AATCAAAGGACCGAGAAGGACCAACT GATCACCTTGAATCTGCTTGTCTCTTAATCTTC	581
	GAAGATTAAGAGGACAAGCAGATTCAAGGTGATCAGTTGGTC CTTCTCGGTCCTTTGATTGTTTAATAAGATCAAATAAAGGTGA ATCCTATATGAAACATGATGAAATTAACCACATT	582
	TTATTAA <u>C</u> AATCAAAG	583
	CTTTGATTGTTTAATAA	584
Retinoblastoma Arg579Term CGA to TGA	ATTTATCATGTTTCATATAGGATTACCTTTATTTGATCTTAT TAAACAATCAAAGGAC <u>C</u> GAGAAGGACCAACTGATCACCTTGA ATCTGCTTGTCTCTTAATCTTCTCTCCAGAATA	585
	TATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAAGGT GATCAGTTGGTCCTTCTC <u>G</u> GTCCTTTGATTGTTTAATAAGATC AAATAAAGGTGAATCCTATATGAAACATGATGAAAT	586
	CAAAGGAC <u>C</u> GAGAAGGA	587
	TCCTTCTC <u>G</u> GTCCTTTG	588
Retinoblastoma Glu580Term GAA to TAA	TCATCATGTTTCATATAGGATTACCTTTATTTGATCTTATTAA ACAATCAAAGGACCGAG <u>A</u> AGGACCAACTGATCACCTTGAATC TGCTTGTCTCTTAATCTTCTCTCCAGAATAATC	589
	GATTATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAA GGTGATCAGTTGGTCCTTCTC <u>G</u> GTCCTTTGATTGTTTAATAAG ATCAAATAAAGGTGAATCCTATATGAAACATGATGA	590
	AGGACCGAG <u>A</u> AGGACCA	591
	TGGTCCTTCTC <u>G</u> GTCCT	592
Retinoblastoma Ser634Term TCA to TGA	AGAAAAAGGTTCAACTACGCGTGTAATTCTACTGCAAATG CAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGG	593
	CCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCAATGGCT TCTGGGTCTGGAAGGCTGAGGTTGCTTGTGTCTCTGCATTTG CAGTAGAATTTACACGCGTAGTTGAACCTTTTTTCT	594
	AGCAACCTCAGCCTTCC	595
	GGAAGGCTGAGGTTGCT	596

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Ala635Pro GCC to CCC	AAAAAAGGTTCAACTACGCGTGTAATTCTACTGCAAATGCA GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATT GAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGGTT	597
	AACCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCAATGG CTTCTGGGTCTGGAAGGCTGAGGTTGCTTGTGTCTCTGCATT TGCAGTAGAATTTACACGCGTAGTTGAACCTTTTTT	598
	CAACCTCAGCCTTCCAG	599
	CTGGAAGGCTGAGGTTG	600
Retinoblastoma Gln639Term CAG to TAG	ACTACGCGTGTAATTCTACTGCAAATGCAGAGACACAAGCA ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCT CTTTCACTGTTTTATAAAAAAGGTTAGTAGATGATTA	601
	TAATCATCTACTAACCTTTTTTATAAAACAGTGAAAGAGAGGT AGATTTCAATGGCTTCTGGGTCTGGAAGGCTGAGGTTGCTTG TGTCTCTGCATTTGCAGTAGAATTACACGCGTAGT	602
	TCCAGACCCAGAAGCCA	603
	TGGCTTCTGGGTCTGGA	604
Retinoblastoma Leu657Pro CTA to CCA	TTGTAATTCAAATGAACAGTAAAAATGACTAATTTTTCTTATT CCCACAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTT TGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGA	605
	TCTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAAGTGTA TTTAGCCGGAGATAGGCTAGCCGATACACTGTGGGAATAAG AAAAATTAGTCATTTTTACTGTTCATTTTGAATTACAA	606
	GTATCGGCTAGCCTATC	607
	GATAGGCTAGCCGATAC	608
Retinoblastoma Arg661Trp CGG to TGG	AATGAACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGTA TCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCT TCTGTCTGAGCACCCAGAATTAGAACATATCATCT	609
	AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGTATTTAGCCGGAGATAGGCTAGCCGATACACTG TGGGAATAAGAAAAATTAGTCATTTTTACTGTTCAAT	610
	CCTATCTCCGGCTAAAT	611
	ATTTAGCCGGAGATAGG	612
Retinoblastoma Leu662Pro CTA to CCA	AACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGTATCG GCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCT GTCTGAGCACCCAGAATTAGAACATATCATCTGGAC	613

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTCCAGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGG CGTTCACAAAGTGTATTTAGCCGGAGATAGGCTAGCCGATAC ACTGTGGGAATAAGAAAAATTAGTCATTTTTACTGTT	614
	TCTCCGGCTAAATACAC	615
	GTGTATTTAGCCGGAGA	616
Retinoblastoma Glu675Term GAA to TAA	TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACC CTTTCCAGCACACCCTGCAGAATGAGTATGAACTCA	617
	TGAGTTCATACTCATTCTGCAGGGTGTGCTGGAAAAGGGTCC AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGTATTTAGCCGGAGATAGGCTAGCCGATA	618
	AGCACCCAGAATTAGAA	619
	TTCTAATTCTGGGTGCT	620
Retinoblastoma Gln685Pro CAG to CCG	TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATG AACTCATGAGAGACAGGCATTTGGACCAAGTAAGAAA	621
	TTTCTTACTTGGTCCAAATGCCTGTCTCTCATGAGTTCATACT CATTCTGCAGGGTGTGCTGGAAAAGGGTCCAGATGATATGTT CTAATTCTGGGTGCTCAGACAGAAGGCGTTACAAA	622
	CCTTTTCCAGCACACCC	623
	GGGTGTGCTGGAAAAGG	624
Retinoblastoma Cys706Tyr TGT to TAT	AAAACCATGTAATAAAATTCTGACTACTTTTACATCAATTTATT TACTAGATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA AGAATATAGACCTTAAATTCAAATCATTGTAAC	625
	GTTACAATGATTTTGAATTTAAGGTCTATATTCTTCACTTTGCA TATGCCATACATGGAACACATCATAATCTAGTAAATAAATTGA TGTAAGTAGTCAGAATTTTATTACATGGTTTT	626
	TATGATGTGTTCCATGT	627
	ACATGGAACACATCATA	628
Retinoblastoma Cys712Arg TGC to CGC	TTCTGACTACTTTTACATCAATTTATTTACTAGATTATGATGTG TTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA TTCAAATCATTGTAACAGCATACAAGGATCTTC	629
	GAAGATCCTTGTATGCTGTTACAATGATTTTGAATTTAAGGTC TATATTCTTCACTTTGCATATGCCATACATGGAACACATCATA ATCTAGTAAATAAATTGATGTAAAAGTAGTCAGAA	630

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGGCATATGCAAAGTG	631
	CACTTTGCATATGCCAT	632
Retinoblastoma Tyr728Term TAC to TAA	GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAA ATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTGAG GAGGTAGGTAATTTTCCATAGTAAGTTTTTTTGATA	633
	TATCAAAAAA CTT ACTATGGAAAATTACCTACCTCCTGAACA GCATGAGGAAGATCCTTGTATGCTGTTACAATGATTTTGAATT TAAGGTCTATATTCTTCACTTTGCATATGCCATAC	634
	ACAGCATACAAGGATCT	635
	AGATCCTTGTATGCTGT	636
Retinoblastoma Glu748Term GAG to TAG	TTTTTTTTTTTTTTACTGTTCTTCCTCAGACATTCAAACGTGT TTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATA ACTCGGTCTTCATGCAGAGACTGAAAACAAATA	637
	TATTTGTTTTCAGTCTCTGCATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACTCCTCTTCTTTGATCAAAACACGTTTGA ATGTCTGAGGAAGAACAGTAAAAAAAAAAAAAAAA	638
	AAGAAGAGGAGTATGAT	639
	ATCATACTCCTCTTCTT	640
Retinoblastoma Gln762Term CAG to TAG	GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCT ATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCA GTATGCTTCCACCAGGGTAGGTCAAAGTATCCTT	641
	AAGGATACTTTTGACCTACCCTGGTGGAGCATACTGCAAAA TATTTGTTTTCAGTCTCTGCATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACTCCTCTTCTTTGATCAAAAC	642
	TCTTCATGCAGAGACTG	643
	CAGTCTCTGCATGAAGA	644
Retinoblastoma Arg787Term CGA-TGA	TAATCTACTTTTTGTTTTGCTCTAGCCCCCTACCTTGTCAC CAATACCTCACATTCTCGAAGCCCTTACAAGTTTCCTAGTTC ACCCTTACGGATTCTGGAGGGAACATCTATATT	645
	AAATATAGATGTTCCCTCCAGGAATCCGTAAGGGTGAAGTAG GAACTTGTAAGGGCTTCGAGGAATGTGAGGTATTGGTGACA AGGTAGGGGGCTAGAGCAAAAACAAAAAGTAGATTA	646
	ACATTCCTCGAAGCCCT	647
	AGGGCTTCGAGGAATGT	648

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Retinoblastoma Ser816Term TCA to TGA	CCTTACGGATTCTCTGGAGGGAACATCTATATTTACCCCTGA AGAGTCCATATAAAATTTGAGAAGGTCTGCCAACACCAACAA AAATGACTCCAAGATCAAGGTGTGTGTTTTCTCTTA	649
	TAAAGAGAAAACACACACCTTGATCTTGGAGTCATTTTTGTTG GTGTTGGCAGACCTTCTGAAATTTATATGGACTCTTCAGGG GTGAAATATAGATGTTCCCTCCAGGAATCCGTAAGG	650
	TAAATTTGAGAAGGTC	651
	GACCTTCTGAAATTTA	652

EXAMPLE 8

BRCA1 and BRCA2

Breast cancer is the second major cause of cancer death in American women, with an estimated 44,190 lives lost (290 men and 43,900 women) in the US in 1997. While ovarian cancer accounts for fewer deaths than breast cancer, it still represents 4% of all female cancers. In 1994, two breast cancer susceptibility genes were identified: BRCA1 on chromosome 17 and BRCA2 on chromosome 13. When a woman carries a mutation in either BRCA1 or BRCA2, she is at increased risk of being diagnosed with breast or ovarian cancer at some point in her life.

Ford *et al.*, *Am. J. Hum. Genet.* 62: 676-689 (1998) assessed the contribution of BRCA1 and BRCA2 to inherited breast cancer by linkage and mutation analysis in 237 families, each with at least 4 cases of breast cancer. Families were included without regard to the occurrence of ovarian or other cancers. Overall, disease was linked to BRCA1 in an estimated 52% of families, to BRCA2 in 32% of families, and to neither gene in 16%, suggesting other predisposition genes. The majority (81%) of the breast-ovarian cancer families were due to BRCA1, with most others (14%) due to BRCA2. Conversely, the majority (76%) of families with both male and female breast cancer were due to BRCA2. The largest proportion (67%) of families due to other genes were families with 4 or 5 cases of female breast cancer only.

More than 75% of the reported mutations in the BRCA1 gene result in truncated proteins. Couch *et al.*, *Hum. Mutat.* 8: 8-18, 1996. (1996) reported a total of 254 BRCA1 mutations, 132 (52%) of which were unique. A total of 221 (87%) of all mutations or 107 (81%) of the unique mutations are small deletions, insertions, nonsense point mutations, splice variants, and regulatory mutations that result in

truncation or absence of the BRCA1 protein. A total of 11 disease-associated missense mutations (5 unique) and 21 variants (19 unique) as yet unclassified as missense mutations or polymorphisms had been detected. Thirty-five independent benign polymorphisms had been described. The most common mutations were 185delAG and 5382insC, which accounted for 30 (11.7%) and 26 (10.1%), respectively, of all the mutations.

Most BRCA2 mutations are predicted to result in a truncated protein product. The smallest known cancer-associated deletion removes from the C terminus only 224 of the 3,418 residues constituting BRCA2, suggesting that these terminal amino acids are critical for BRCA2 function. Studies (Spain *et al.*, Proc. Natl. Acad. Sci. 96:13920-13925 (1999)) suggest that such truncations eliminate or interfere with 2 nuclear localization signals that reside within the final 156 residues of BRCA2, suggesting that the vast majority of BRCA2 mutants are nonfunctional because they are not translocated into the nucleus.

The attached table discloses the correcting oligonucleotide base sequences for the BRCA1 and BRCA2 oligonucleotides of the invention.

Table 14
BRCA1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Met-1-Ile ATG to ATT	CTGCGCTCAGGAGGCCTTCACCCTCTGCTCTGGGTAAAGTT CATTGGAACAGAAAGAAATGGATTATCTGCTCTTCGCGTTG AAGAAGTACAAAATGTCATTAATGCTATGCAGAAAATC	653
	GATTTTCTGCATAGCATTAAATGACATTTTGTACTTCTTCAACG CGAAGAGCAGATAAATCCATTCTTTCTGTTCCAATGAACTTT ACCCAGAGCAGAGGGTGAAGGCCTCCTGAGCGCAG	654
	AAAGAAATGGATTATC	655
	GATAAATCCATTCTTT	656
Breast Cancer Val-11-Ala GTA to GCA	CTGGGTAAAGTTCATTGGAACAGAAAGAAATGGATTATCTG CTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGCA GAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGAT	657
	ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCTGCATA GCATTAATGACATTTTGTACTTCTTCAACGCGAAGAGCAGATA AATCCATTCTTTCTGTTCCAATGAACTTTACCCAG	658
	TGAAGAAGTACAAAATG	659

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATTTTGTACTTCTTCA	660
Breast Cancer Ile-21-Val ATC to GTC	ATGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCA TTAATGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGG AGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	661
	GGTCACACTTTGTGGAGACAGGTTCTTGATCAACTCCAGAC AGATGGGACACTCTAAGATTTTCTGCATAGCATTAAATGACATT TTGTACTTCTTCAACGCGAAGAGCAGATAAATCCAT	662
	TGCAGAAAATCTTAGAG	663
	CTCTAAGATTTTCTGCA	664
Breast Cancer Leu-22-Ser TTA to TCA	ATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAA TGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTT GATCAAGGAACCTGTCTCCACAAAGTGTGACCACAT	665
	ATGTGGTCACACTTTGTGGAGACAGGTTCTTGATCAACTCC AGACAGATGGGACACTCTAAGATTTTCTGCATAGCATTAAATG ACATTTTGTACTTCTTCAACGCGAAGAGCAGATAAAT	666
	GAAAATCTTAGAGTGTC	667
	GACACTCTAAGATTTTC	668
Breast Cancer Cys-39-Tyr TGT to TAT	AGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGG AACCTGTCTCCACAAAGTGTGACCACATATTTTGCAAATTTTG CATGCTGAACTTCTCAACCAGAAGAAAGGGCCTTC	669
	GAAGGCCCTTTCTTCTGGTTGAGAAGTTTCAGCATGCAAAT TTGCAAATATGTGGTCACACTTTGTGGAGACAGGTTCTTG ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCT	670
	CACAAAGTGTGACCACA	671
	TGTGGTCACACTTTGTG	672
Breast Cancer Cys-61-Gly TGT to GGT	CACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACCAGA AGAAAGGGCCTTCACAGTGTCTTTATGTAAGAATGATATAAC CAAAGGAGCCTACAAGAAAGTACGAGATTAGTC	673
	GACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGGTTATATC ATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTTCTGGTT GAGAAGTTTCAGCATGCAAATTTGCAAATATGTG	674
	CTTCACAGTGTCTTTA	675
	TAAAGGACACTGTGAAG	676

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Leu-63-Stop TTA to TAA	TTTGCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGG GCCTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGG AGCCTACAAGAAAGTACGAGATTTAGTCAACTTGT	677
	ACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGG TTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTT CTGGTTGAGAAGTTTCAGCATGCAAATTTGCAA	678
	GTGTCCTTTATGTAAGA	679
	TCTTACATAAAGGACAC	680
Breast Cancer Cys-64-Arg TGT to CGT	TGCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGGG CCTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGGA GCCTACAAGAAAGTACGAGATTTAGTCAACTTGTG	681
Breast Cancer Cys-64-Gly TGT to GGT	CAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTT GGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTC TTCTGGTTGAGAAGTTTCAGCATGCAAATTTGCA	682
	GTCCTTTATGTAAGAAT	683
	ATTCTTACATAAAGGAC	684
Breast Cancer Cys-64-Tyr TGT to TAT	GCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGGGC CTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGGAG CCTACAAGAAAGTACGAGATTTAGTCAACTTGTGTA	685
	TCAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTT TGGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTT CTTCTGGTTGAGAAGTTTCAGCATGCAAATTTGC	686
	TCCTTTATGTAAGAATG	687
	CATTCTTACATAAAGGA	688
Breast Cancer Gln-74-Stop CAA to TAA	CAGAAGAAAGGGCCTTCACAGTGTCTTTATGTAAGAATGAT ATAACCAAAGGAGCCTACAAGAAAGTACGAGATTTAGTCAA CTTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTC	689
	GAAAGCACAAATGATTTTCAATAGCTCTTCAACAAGTTGACT AAATCTCGTACTTTCTTGTAGGCTCCTTTTGGTTATATCATTCT TACATAAAGGACACTGTGAAGGCCCTTTCTTCTG	690
	GGAGCCTACAAGAAAGT	691
	ACTTTCTTGTAGGCTCC	692

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Tyr-105-Cys TAT to TGT	AGCTATTGAAAATCATTGTGCTTTTCAGCTTGACACAGGTTT GGAGTATGCAAACAGCTATAATTTTGCAAAAAGGAAAATAAC TCTCCTGAACATCTAAAAGATGAAGTTTCTATCAT	693
	ATGATAGAACTTCATCTTTTAGATGTTTCAGGAGAGTTATTTT CCTTTTTTGCAAATTATAGCTGTTTGCATACTCCAAACCTGT GTCAAGCTGAAAAGCACAAATGATTTTCAATAGCT	694
	AAACAGCTATAATTTTG	695
	CAAAATTATAGCTGTTT	696
Breast Cancer Asn-158-Tyr AAC to TAC	CTACAGAGTGAACCCGAAAATCCTTCCTTGACAGGAAACCAGT CTCAGTGTCCAACCTCTTAACCTTGGAAGTGTGAGAACTCTG AGGACAAAGCAGCGGATACAACCTCAAAGACGTCTG	697
	CAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAG TTCTCACAGTTCCAAGGTTAGAGAGTTGGACACTGAGACTGG TTTCCTGCAAGGAAGGATTTTCGGGTTCACTCTGTAG	698
	AACTCTCTAACCTTGGA	699
	TCCAAGGTTAGAGAGTT	700
Breast Cancer Gln-169-Stop CAG to TAG	GAAACCAGTCTCAGTGTCCAACCTCTTAACCTTGGAAGTGTG AGAAGTCTGAGGACAAAGCAGCGGATACAACCTCAAAGAC GTCTGTCTACATTGAATTGGGATCTGATTCTTCTGAAG	701
	CTTCAGAAGAATCAGATCCCAATTCAATGTAGACAGACGTCTT TTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCACAGT TCCAAGGTTAGAGAGTTGGACACTGAGACTGGTTTC	702
	GGACAAAGCAGCGGATA	703
	TATCCGCTGCTTTGTCC	704
Breast Cancer Trp-353-Stop TGG to TAG	CTCCCAGCACAGAAAAAAGGTAGATCTGAATGCTGATCCCC TGTGTGAGAGAAAAGAATGGAATAAGCAGAACTGCCATGCT CAGAGAATCCTAGAGATACTGAAGATGTTCTTGGAT	705
	ATCCAAGGAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT GGCAGTTTCTGCTTATTCCATTCTTTCTCTCACACAGGGGAT CAGCATTGAGATCTACCTTTTTTCTGTGCTGGGAG	706
	AAAAGAATGGAATAAGC	707
	GCTTATTCCATTCTTT	708
Breast Cancer Ile-379-Met ATT to ATG	ATGCTCAGAGAATCCTAGAGATACTGAAGATGTTCTTGGAT AACACTAAATAGCAGCATTCAGAAAGTTAATGAGTGGTTTTCC AGAAGTGATGAACTGTTAGGTTCTGATGACTCACAT	709

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGTGAGTCATCAGAACCTAACAGTTCATCACTTCTGGAAAC CACTCATTAACTTTCTGAATGCTGCTATTTAGTGTTATCCAAG GAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT	710
	AGCAGCATT <u>C</u> AGAAAGT	711
	ACTTTCTGAATGCTGCT	712
Breast Cancer Glu-421-Gly GAA to GGA	GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTATTGGACG TTCTAAATGAGGTAGATGAATATTCTGGTTCTTCAGAGAAAAT AGACTTACTGGCCAGTGATCCTCATGAGGCTTTAAT	713
	ATTAAAGCCTCATGAGGATCACTGGCCAGTAAGTCTATTTTCT CTGAAGAACCAGAATATTCATCTACCTCATTTAGAACGTCCAA TACATCAGCTACTTTGGCATTGATTGAGACTCCC	714
	GGTAGATGAATATTCTG	715
	CAGAATATTCATCTACC	716
Breast Cancer Phe-461-Leu TTT to CTT	ATATGTAAAAGTGAAAGAGTTCCTCCAAATCAGTAGAGAGTA ATATTGAAGACAAAATATTTGGGAAAACCTATCGGAAGAAGG CAAGCCTCCCCAACTTAAGCCATGTAAGTGAATC	717
	GATTTTCAGTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCT TCCGATAGGTTTTCCCAAATATTTTGTCTTCAATATTACTCTCT ACTGATTGGAGTGAAGTCTTTCATTTTACATAT	718
	ACAAAATATTTGGGAAA	719
	TTTCCCAAATATTTTGT	720
Breast Cancer Tyr-465-Leu TAT to GAT	GAAAGAGTTCCTCCAAATCAGTAGAGAGTAATATTGAAGAC AAAATATTTGGGAAAACCTATCGGAAGAAGGCAAGCCTCCCC AACTTAAGCCATGTAAGTGAATCTAATTATAGGAG	721
	CTCCTATAATTAGATTTTCAGTTACATGGCTTAAGTTGGGGAG GCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCA ATATTACTCTCTACTGATTGGAGTGAAGTCTTTC	722
	GGAAAACCTATCGGAAG	723
	CTTCCGATAGGTTTTCC	724
Breast Cancer Gly-484-Stop GGA to TGA	ACCTATCGGAAGAAGGCAAGCCTCCCCAACTTAAGCCATGTA ACTGAAAATCTAATTATAGGAGCATTTGTTACTGAGCCACAGA TAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC	725
	GCTTTAATTTATTTGTGAGGGGACGCTCTTGTATTATCTGTGG CTCAGTAACAAATGCTCCTATAATTAGATTTTCAGTTACATGG CTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGT	726

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATTATAGGAGCATT	727
	AAATGCTCCTATAATTA	728
Breast Cancer Arg-507-Ile AGA to ATA	T TACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATA AATTAAAGCGTAAAAGGAGACCTACATCAGGCCTTCATCCTG AGGATTTTATCAAGAAAGCAGATTGGCAGTTCAAAA	729
	TTTTGAACTGCCAAATCTGCTTTCTTGATAAAATCCTCAGGAT GAAGGCCTGATGTAGGTCTCCTTTTACGCTTTAATTTATTTGT GAGGGGACGCTCTTGATTATCTGTGGCTCAGTAA	730
	TAAAAGGAGACCTACAT	731
	ATGTAGGTCTCCTTTTA	732
Breast Cancer Ser-510-Stop TCA to TGA	CACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC GTAAAAGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTA TCAAGAAAGCAGATTGGCAGTTCAAAGACTCCTGA	733
	TCAGGAGTCTTTTGAAGTCCAAATCTGCTTTCTTGATAAAAT CCTCAGGATGAAGGCCTGATGTAGGTCTCCTTTTACGCTTTA ATTTATTTGTGAGGGGACGCTCTTGATTATCTGTG	734
	ACCTACATCAGGCCTTC	735
	GAAGGCCTGATGTAGGT	736
Breast Cancer Gln-526-Stop CAA to TAA	AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTGGCAGTTCAAAGACTCCTGAAATGATAAATC AGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA	737
	TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTTGAAGTCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT	738
	TGGCAGTTCAAAGACT	739
	AGTCTTTTGAAGTCCCA	740
Breast Cancer Gln-541-Stop CAG to TAG	AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTGGCAGTTCAAAGACTCCTGAAATGATAAATC AGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA	741
	TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTTGAAGTCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT	742
	AAACGGAGCAGAATGGT	743
	ACCATTCTGCTCCGTTT	744

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Breast Cancer Gly-552-Val GGT to GTT	TAAATCAGGGA ACT AACCAAACGGAGCAGAATGGTCAAGTGA TGAATATTACTAATAGTGGTCATGAGAATAAAACAAAAGGTGA TTCTATTCAGAATGAGAAAAATCCTAACCCAATAGA	745
	TCTATTGGGTAGGATTTTTCTCATTCTGAATAGAATCACCTTT TGTTTTATTCTCATGACCACTATTAGTAATATTCATCACTTGAC CATTCTGCTCCGTTTGGTTAGTTCCTGATTTA	746
	TAATAGTGGTCATGAGA	47
	TCTCATGACCACTATTA	748
Breast Cancer Gln-563-Stop CAG to TAG	GGTCAAGTGATGAATATTACTAATAGTGGTCATGAGAATAAAA CAAAGGTGATTCTATTCAGAATGAGAAAAATCCTAACCCAAT AGAATCACTCGAAAAAGAATCTGCTTTCAAACGA	749
	TCGTTTTGAAAGCAGATTCTTTTCGAGTGATTCTATTGGGT AGGATTTTTCTCATTCTGAATAGAATCACCTTTTGTATTCT CATGACCACTATTAGTAATATTCATCACTTGACC	750
	ATTCTATTCAGAATGAG	751
	CTCATTCTGAATAGAAT	752
Ovarian Cancer Lys-607-Stop AAA to TAA	ATAAGCAGCAGTATAAGCAATATGGA ACT CGAATTAAATATCC ACAATTCAAAGCACCTAAAAAGAATAGGCTGAGGAGGAAGT CTTCTACCAGGCATATTCATGCGCTTGA ACT AGTAG	753
	CTACTAGTTCAAGCGCATGAATATGCCTGGTAGAAGACTTCC TCCTCAGCCTATTCTTTTAGGTGCTTTTGAATTGTGGATATT TAATTCGAGTTCCATATTGCTTATACTGCTGCTTAT	754
	AAGCACCTAAAAAGAAT	755
	ATTCTTTTAGGTGCTT	756
Breast Cancer Leu-639-Stop TTG to TAG	ATATTCATGCGCTTGA ACT AGTAGTCAGTAGAAATCTAAGCCC ACCTAATTGACTGAATTGCAAATTGATAGTTGTTCTAGCAGT GAAGAGATAAAGAAAAAAGTACAACCAAATGCC	757
	GGCATTGGTTGTACTTTTTTTCTTTATCTCTTCACTGCTAGA ACA ACT TATCAATTTGCAATTCAGTACAATTAGGTGGGCTTAGA TTTCTACTGACTACTAGTTCAAGCGCATGAATAT	758
	TACTGAATTGCAAATTG	759
	CAATTTGCAATTCAGTA	760
Breast Cancer Asp-693-Asn GAC to AAC	GAACCTGCAACTGGAGCCAAGAAGAGTAACAAGCCAAATGAA CAGACAAGTAAAGACATGACAGCGATACTTTCCAGAGCTG AAGTTAACAAATGCACCTGGTTCTTTTACTAAGTGTT	761

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AACACTTAGTAAAGAACCAGGTGCATTTGTTAACTTCAGCTC TGGGAAAGTATCGCTGT <u>C</u> ATGTCTTTTACTTGTCTGTTCAATT GGCTTGTTACTCTTCTTGGCTCCAGTTGCAGGTT	762
	AAAGACAT <u>G</u> ACAGCGAT	763
	ATCGCTGT <u>C</u> ATGTCTTT	764
Ovarian Cancer Glu-720-Stop GAA to TAA	CTGAAGTTAAACAATGCACCTGGTTCTTTACTAAGTGTTCAA ATACCAGTGAACCTTAAAG <u>A</u> ATTTGTCAATCCTAGCCTTCCAAG AGAAGAAAAAGAAGAGAACTAGAAACAGTTAAAG	765
	CTTTAACTGTTTCTAGTTTCTCTTCTTTTCTTCTCTTGAAGG CTAGGATTGACAAATT <u>C</u> TTTAAGTTCACTGGTATTTGAACACT TAGTAAAGAACCAGGTGCATTTGTTAACTTCAG	766
	AACTTAAAG <u>A</u> ATTTGTC	767
	GACAAATT <u>C</u> TTTAAGTT	768
Breast Cancer Glu-755-Stop GAA to TAA	CTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAA GATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAAGTAAAGA TCTGTAGAGAGTAGCAGTATTTCAATTGGTACCTGGTA	769
	TACCAGGTACCAATGAAATACTGCTACTCTCTACAGATCTTTC AGTTTGCAAACCCTTT <u>C</u> TCCACTTAACATGAGATCTTTGGGG TCTTCAGCATTATTAGACACTTTAACTGTTTCTAG	770
	TAAGTGGAGAAAGGGTT	771
	AACCCTTT <u>C</u> TCCACTTA	772
Breast Cancer Ser-770-Stop TCA to TAA	TCATGTTAAGTGGAGAAAGGGTTTTGCAAAGTAAAGATCTG TAGAGAGTAGCAGTATTT <u>C</u> ATTGGTACCTGGTACTGATTATG GCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCAC	773
	GTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAA TCAGTACCAGGTACCAAT <u>G</u> AAATACTGCTACTCTCTACAGAT CTTTCAGTTTGCAAACCCTTTCTCCACTTAACATGA	774
	CAGTATTT <u>C</u> ATTGGTAC	775
	GTACCAAT <u>G</u> AAATACTG	776
Breast Cancer Val-772-Ala GTA to GCA	TAAGTGGAGAAAGGGTTTTGCAAAGTAAAGATCTGTAGAGA GTAGCAGTATTTCAATTGGT <u>A</u> CTGGTACTGATTATGGCACTC AGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGG	777
	CCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTG CCATAATCAGTACCAGGT <u>A</u> CCAATGAAATACTGCTACTCTCTA CAGATCTTTCAGTTTGCAAACCCTTTCTCCACTTA	778

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTCATTGGT <u>T</u> ACCTGGTA	779
	TACCAGGT <u>A</u> CCAATGAA	780
Breast Cancer Gln-780-Stop CAG to TAG	ACTGAAAGATCTGTAGAGAGTAGCAGTATTTTATTGGTACCT GGTACTGATTATGGCACT <u>C</u> AGGAAAGTATCTCGTTACTGGAA GTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATA	781
	TATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAG TAACGAGATACTTTCTGAGTGCCATAATCAGTACCAGGTAC CAATGAAATACTGCTAGTCTCTACAGATCTTTCAGT	782
	ATGGCACT <u>C</u> AGGAAAGT	783
	ACTTTCCTGAGTGCCAT	784
Breast Cancer Glu-797-Stop GAA to TAA	TATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACT CTAGGGAAGGCAAAAACAGAACCAATAAATGTGTGAGTCAG TGTGCAGCATTGAAAACCCCAAGGGACTAATTCATG	785
	CATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGAC TCACACATTTATTTGGTT <u>C</u> TGTTTTTGCCTTCCCTAGAGTGCT AACTTCCAGTAACGAGATACTTTCCTGAGTGCCATA	786
	CAAAAACAGAACCAAT	787
	ATTTGGTT <u>C</u> TGTTTTTG	788
Breast Cancer Lys-820-Glu AAA to GAA	AAATGTGTGAGTCAGTGTGCAGCATTGAAAACCCCAAGGGA CTAATTCATGGTTGTTCCA <u>A</u> AGATAATAGAAATGACACAGAAG GCTTTAAGTATCCATTGGGACATGAAGTTAACCACA	789
	TGTGGTTAACTTCATGTCCCAATGGATACTTAAAGCCTTCTGT GTCATTTCTATTATCTT <u>G</u> GGAACAACCATGAATTAGTCCCTTG GGGTTTTCAAATGCTGCACACTGACTCACACATTT	790
	GTTGTTCCA <u>A</u> AGATAAT	791
	ATTATCTTTGGAACAAC	792
Breast Cancer Thr-826-Lys ACA to AAA	CAGCATTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCA AAGATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGG GACATGAAGTTAACCACAGTCGGGAAACAAGCATAGA	793
	TCTATGCTTGTTTCCCGACTGTGGTTAACTTCATGTCCCAATG GATACTTAAAGCCTTCTG <u>T</u> GTGCAATTTCTATTATCTTTGGAACA ACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTG	794
	AAATGACAC <u>A</u> GAAAGGCT	795
	AGCCTTCTG <u>T</u> GTCATTT	796

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Breast Cancer Arg-841-Trp CGG to TGG	GATAATAGAAATGACACAGAAGGCTTTAAGTATCCATTGGGA CATGAAGTTAACCACAGT <u>C</u> GGGAAACAAGCATAGAAATGGAA GAAAGTGAACCTTGATGCTCAGTATTTGCAGAATACAT	797
	ATGTATTCTGCAAATACTGAGCATCAAGTTCACTTTCTTCCAT TTCTATGCTTGTTCCTCCGACTGTGGTTAACTTCATGTCCCAAT GGATACTTAAAGCCTTCTGTGTCATTTCTATTATC	798
	ACCACAGT <u>C</u> GGGAAACA	799
	TGTTTCCCGACTGTGGT	800
Breast Cancer Pro-871-Leu CCG to CTG	AACTTGATGCTCAGTATTTGCAGAATACATTCAAGGTTTCAAA GCGCCAGTCATTTGCTC <u>C</u> GTTTTCAAATCCAGGAAATGCAGA AGAGGAATGTGCAACATTCTCTGCCCACTCTGGGTC	801
	GACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCA TTTCTTGGAATTTGAAAACGAGCAATGACTGGCGCTTTGAA ACCTTGAATGTATTCTGCAAATACTGAGCATCAAGTT	802
	ATTGCTC <u>C</u> GTTTTCAA	803
	TTGAAAACGAGCAAT	804
Breast Cancer Leu-892-Ser TTA to TCA	TTCAAATCCAGGAAATGCAGAAGAGGAATGTGCAACATTCT CTGCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCA CTTTTGAATGTGAACAAAAGGAAGAAATCAAGGAAA	805
	TTTCCTTGATTTTCTTCCTTTTGTTACATTCAAAGTGACTTT TGGACTTTGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGT TGCACATTCCTCTTCTGCATTTCTGGATTTGAAA	806
	TGGGTCCTTAAAGAAAC	807
	GTTTCTTTAAGGACCCA	808
Breast Cancer Glu-908-Stop GAA to TAA	CACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTTTTG AATGTGAACAAAAGGAAGAAAATCAAGGAAAGAATGAGTCTA ATATCAAGCCTGTACAGACAGTTAATATCACTGCAG	809
	CTGCAGTGATATTAAGTGTCTGTACAGGCTTGATATTAGACTC ATTCTTTCCTTGATTTTCTTCCTTTTGTTACATTCAAAGTGA CTTTTGACTTTGTTTCTTTAAGGACCCAGAGTG	810
	AAAAGGAAGAAAATCAA	811
	TTGATTTTCTTCCTTTT	812
Breast Cancer Gly-960-Asp GGC to GAC	ATAATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTTGTCT ATCATCTCAGTTCAGAGGCAACGAACTGGACTCATTACTCC AAATAACATGGACTTTTACAAAACCATATCGTAT	813

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATACGATATGGGTTTTGTAAAAGTCCATGTTTATTTGGAGTAA TGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAA ACCTAGAGCCTCCTTTGATACTACATTTGGCATTAT	814
	G TTCAGAGGCAACGAAA	815
	TTTCGTTGCCTCTGAAC	816
Breast Cancer Met-1008-Ile ATG to ATA	ATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGGAAAAC TTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAAT GAGAACATTCCAAGTACAGTGAGCACAATTAGCCGT	817
	ACGGCTAATTGTGCTCACTGTACTTGAATGTTCTCATTTCCC ATTTCTCTTTCAGGTGACATTGAATGTTCTCAAAGTTTTCT CTAGCAGATTTTTCTTACATTAGTTTTAACAAAT	818
	CATTCAATGTCACCTGA	819
	TCAGGTGACATTGAATG	820
Breast Cancer Thr-1025-Ile ACA to ATA	ACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAA ATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATA ACATTAGAGAAAATGTTTTAAAGAAGCCAGCTCAAG	821
	CTTGAGCTGGCTTCTTTAAAACATTTTCTCTAATGTTATTACG GCTAATTGTGCTCACTGTACTTGAATGTTCTCATTTCCCAT TCTCTTTCAGGTGACATTGAATGTTCTCAAAGT	822
	TCCAAGTACAGTGAGCA	823
	TGCTCACTGTACTTGGA	824
Breast Cancer Glu-1038-Gly GAA to GGA	ACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAG AGAAAATGTTTTTAAAGAAGCCAGCTCAAGCAATATTAATGAA GTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTAT	825
	ATACTGGAGCCCACTTCATTAGTACTGGAACCTACTTCATTAA TATTGCTTGAGCTGGCTTCTTTAAAACATTTCTCTAATGTTA TTACGGCTAATTGTGCTCACTGTACTTGGAATGT	826
	TTTTAAAGAAGCCAGCT	827
	AGCTGGCTTCTTTAAAA	828
Breast Cancer Ser-1040-Asn AGC to AAC	CAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAA ATGTTTTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGG TTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA	829
	TCATTAATACTGGAGCCCACTTCATTAGTACTGGAACCTACTT CATTAATATTGCTTGAGCTGGCTTCTTTAAAACATTTTCTCTA ATGTTATTACGGCTAATTGTGCTCACTGTACTTG	830

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AGAAGCCAGCTCAAGCA	831
	TGCTTGAGCTGGCTTCT	832
Breast Cancer Val-1047-Ala GTA to GCA	GCCGTAATAACATTAGAGAAAATGTTTTAAAGAAGCCAGCTC AAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGG CTCCAGTATTAATGAAATAGGTTCCAGTGATGAAAA	833
	TTTTCATCACTGGAACCTATTTCAATTAATACTGGAGCCCACTT CATAGTACTGGAACCTACTTCATTAATATTGCTTGAGCTGGC TTCTTTAAAAACATTTTCTCTAATGTTATTACGGC	834
	TAATGAAGTAGGTTCCA	835
	TGGAACCTACTTCATTA	836
Breast Cancer Leu-1080-Stop TTG to TAG	AAATAGGTTCCAGTGATGAAAACATTCAAGCAGAACTAGGTA GAAACAGAGGGCCAAAATGAATGCTATGCTTAGATTAGGGG TTTTGCAACCTGAGGTCTATAACAAAGTCTTCCTGG	837
	CCAGGAAGACTTTGTTTATAGACCTCAGGTTGCAAAACCCCT AATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTA GTTCTGCTTGAATGTTTTCATCACTGGAACCTATTT	838
	GCCAAAATGAATGCTA	839
	TAGCATTCAATTTTGGC	840
Breast Cancer Leu-1086-Stop TTA to TGA	AAACATTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAAT TGAATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCT ATAACAAAGTCTTCCTGGAAGTAATTGTAAGCATCC	841
	GGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCT CAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTG GCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTT	842
	GCTTAGATTAGGGGTTT	843
	AAACCCCTAATCTAAGC	844
Breast Cancer Ser-1130-Stop TCA to TGA	AGCAAGAATATGAAGAAGTAGTTCAGACTGTTAATACAGATTT CTCTCCATATCTGATTTGAGATAACTTAGAACAGCCTATGGGA AGTAGTCATGCATCTCAGGTTTGTTCTGAGACACC	845
	GGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCATA GGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCT GTATTAACAGTCTGAACTACTTCTTCATATTCTTGCT	846
	TCTGATTTGAGATAACT	847
	AGTTATCTGAAATCAGA	848

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Breast Cancer Lys-1183-Arg AAA to AGA	CTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTT TAGCAAAAGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTA GCCCTTTCACCCATACACATTTGGCTCAGGGTTACCG	849
	CGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGGGCTAGG ACTCCTGCTAAGCTCTCCTTTCTGGACGCTTTTGCTAAAAACA GCAGAACTTTCCTTAATGTCATTTTCAGCAAACTAG	850
	CGTCCAGAAAGGAGAGC	851
	GCTCTCCTTTCTGGACG	852
Breast Cancer Gln-1200-Stop CAG to TAG	AGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTT CACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGG	853
	CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGG GCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCT	854
	ATTTGGCTCAGGGTTAC	855
	GTAACCCTGAGCCAAAT	856
Breast Cancer Arg-1203-Stop CGA to TGA	AAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACA CATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGAAATTAGA GTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGC	857
	GCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAGGACTCTAA TTTCTTGGCCCCTCTTCGGTAACCCTGAGCCAAATGTGTATG GGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTT	858
	AGGGTTACCGAAGAGGG	859
	CCCTCTTCGGTAACCCT	860
Breast Cancer Glu-1214-Stop GAG to TAG	ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAA GAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGA AGAGCTTCCCTGCTTCCAACACTTGTTATTTGGTAAAG	861
	CTTTACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCAT CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGT	862
	CCTCAGAAGAGAACTTA	863
	TAAGTTCTCTTCTGAGG	864
Breast Cancer Glu-1219-Asp GAG to GAC	TCAGGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAG AAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCC AACACTTGTTATTTGGTAAAGTAAACAATATACCTTCT	865

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTGGAAG CAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAG GACTCTAATTTCTTGGCCCCTCTTCGGTAACCTGA	866
	TCTAGTGAGGATGAAGA	867
	TCTTCATCCTCACTAGA	868
Breast Cancer Glu-1221-Stop GAA to TAA	GGTTACCGAAGAGGGGGCCAAGAAATTAGAGTCCTCAGAAGA GAACTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCCAACA CTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	869
	ACTGAGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTG GAAGCAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTC TGAGGACTCTAATTTCTTGGCCCCTCTTCGGTAACC	870
	GTGAGGATGAAGAGCTT	871
	AAGCTCTTCATCCTCAC	872
Breast Cancer Glu-1250-Stop GAG to TAG	TTATTTGGTAAAGTAAACAATATACCTTCTCAGTCTACTAGGC ATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGG AGAATTTATTATCATTGAAGAATAGCTTAAATGACT	873
	AGTCATTTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTG TTCTTAGACAGACACTCGGTAGCAACGGTGCTATGCCTAGTA GACTGAGAAGGTATATTGTTTACTTTACCAAATAA	874
	TTGCTACCGAGTGTCTG	875
	CAGACACTCGGTAGCAA	876
Breast Cancer Ser-1262-Stop TCA to TAA	CTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACA CAGAGGAGAATTTATTATCATTGAAGAATAGCTTAAATGACTG CAGTAACCAGGTAATATTGGCAAAGGCATCTCAGGA	877
	TCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCAT TTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTGTTCTTA GACAGACACTCGGTAGCAACGGTGCTATGCCTAG	878
	TTTATTATCATTGAAGA	879
	TCTTCAATGATAATAA	880
Breast Cancer Gln-1281-Stop CAG to TAG	TTATCATTGAAGAATAGCTTAAATGACTGCAGTAACCAGGTAA TATTGGCAAAGGCATCTCAGGAACATCACCTTAGTGAGGAAA CAAAATGTTCTGCTAGCTTGTTTTCTTCACAGTGCA	881
	TGCACTGTGAAGAAAACAAGCTAGCAGAACATTTTGTTTCCTC ACTAAGGTGATGTTCTGAGATGCCTTTGCCAATATTACCTG GTTACTGCAGTCATTTAAGCTATTCTTCAATGATAA	882

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGCATCTCAGGAACAT	883
	ATGTTCTTGAGATGCCT	884
Breast Cancer Gln-1313-Stop CAG to TAG	GCTAGCTTGTTTTCTTCACAGTGCAGTGAATTGGAAGACTTG ACTGCAAATACAAACACCCAGGATCCTTTCTTGATTGGTTCTT CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAG	885
	CTCCCTGGCTTTCAGACTGATGCCTCATTTGTTTGAAGAAC CAATCAAGAAAGGATCCTGGGTGTTTGTATTGTCAGTCAAGT CTTCCAATTCAGTCACTGTGAAGAAAACAAGCTAGC	886
	CAAACACCCAGGATCCT	887
	AGGATCCTGGGTGTTTG	888
Breast Cancer Ile-1318-Val ATT to GTT	TCACAGTGCAGTGAATTGGAAGACTTGACTGCAAATACAAAC ACCCAGGATCCTTTCTTGATTGGTTCTTCCAAACAAATGAGG CATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACA	889
	TGTCAGTCAAGACCAACTCCCTGGCTTTCAGACTGATGCCTCA TTTGTTTGAAGAACCAATCAAGAAAGGATCCTGGGTGTTTG TATTGTCAGTCAAGTCTTCCAATTCAGTCACTGTGA	890
	CTTTCTTGATTGGTTCT	891
	AGAACCAATCAAGAAAG	892
Breast Cancer Gln-1323-Stop CAA to TAA	TTGGAAGACTTGACTGCAAATACAAACACCCAGGATCCTTTC TTGATTGGTTCTTCCAAACAAATGAGGCATCAGTCTGAAAGC CAGGGAGTTGGTCTGAGTGACAAGGAATTGGTTTCAG	893
	CTGAAACCAATTCCTTGTCAGTCAAGACCAACTCCCTGGCTTT CAGACTGATGCCTCATTTGTTTGAAGAACCAATCAAGAAAG GATCCTGGGTGTTTGTATTGTCAGTCAAGTCTTCCAA	894
	CTTCCAAACAAATGAGG	895
	CCTCATTTGTTTGAAG	896
Breast Cancer Arg-1347-Gly AGA to GGA	CAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAGGAATT GGTTTCAGATGATGAAGAAAGAGGAACGGGCTTGGAAGAAA ATAATCAAGAAGAGCAAAGCATGGATTCAAACCTTAGGTA	897
	TACCTAAGTTTGAATCCATGCTTTGCTCTTCTTGATTATTTCT TCCAAGCCCGTTCTCTTTCTTCATCATCTGAAACCAATTCCT TGTCAGTCAAGACCAACTCCCTGGCTTTCAGACTG	898
	ATGAAGAAAGAGGAACG	899
	CGTTCCTCTTTCTTCAT	900

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Gln-1395-Stop CAG to TAG	GAAACAAGCGTCTCTGAAGACTGCTCAGGGCTATCCTCTCAG AGTGACATTTTAACCACTCAGGTAAAAAGCGTGTGTGTGTGT GCACATGCGTGTGTGTGGTGTCTTTGCATTTCAGTAG	901
	CTACTGAATGCAAAGGACACCACACACACGCATGTGCACACA CACACACGCTTTTTACCTGAGTGGTTAAATGTCACTCTGAG AGGATAGCCCTGAGCAGTCTTCAGAGACGCTTGTTTC	902
	TAACCACTCAGGTAAAA	903
	TTTTACCTGAGTGGTTA	904
Breast Cancer Gln-1408-Stop CAG to TAG	TGGTGCCATTTATCGTTTTTGAAGCAGAGGGATACCATGCAA CATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAA GCTGTGTTAGAACAGCATGGGAGCCAGCCTTCTAACA	905
	TGTTAGAAGGCTGGCTCCCATGCTGTTCTAACACAGCTTCTA GTTTCAGCCATTTCTGCTGGAGCTTTATCAGGTTATGTTGCAT GGTATCCCTCTGCTTCAAAAACGATAAATGGCACCA	906
	TAAAGCTCCAGCAGGAA	907
	TTCCTGCTGGAGCTTTA	908
Breast Cancer Arg-1443-Gly CGA to GGA	AGCCAGCCTTCTAACAGCTACCCTTCCATCATAAGTGACTCT TCTGCCCTTGAGGACCTGCGAAATCCAGAACAAGCACATCA GAAAAAGGTGTGTATTGTTGGCCAAACACTGATATCT	909
Arg-1443-Stop CGA to TGA	AGATATCAGTGTTTGGCCAACAATACACACCTTTTTCTGATGT GCTTTGTTCTGGATTTGCGAGGTCCTCAAGGGCAGAAGAGTC ACTTATGATGGAAGGGTAGCTGTTAGAAGGCTGGCT	910
	AGGACCTGCGAAATCCA	911
	TGGATTTGCGAGGTCCT	912
Breast Cancer Ser-1512-Ile AGT to ATT	CAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAGGTT GTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC	913
	GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG	914
	AGGAGCAACAGCTGGAA	915
	TTCCAGCTGTTGCTCCT	916
Breast Cancer Gln-1538-Stop CAG to TAG	ATCTTTCTAGGTCATCCCCTTCTAAATGCCCATCATTAGATGA TAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTCAGAATAG AAACTACCATCTCAAGAGGAGCTCATTAAGGTTGT	917

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCT GAAGACTCCCAGAGCAACTGTGCATGTACCACCTATCATCTA ATGATGGGCATTTAGAAGGGGATGACCTAGAAAGAT	918
	CATGCACAGTTGCTCTG	919
	CAGAGCAACTGTGCATG	920
Breast Cancer Glu-1541-Stop GAG to TAG	CAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAAGGTT GTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC	921
	GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG	922
	AGGAGCAACAGCTGGAA	923
	TTCCAGCTGTTGCTCCT	924
Breast Cancer Thr-1561-Ile ACC to ATC	AACTACCCATCTCAAGAGGAGCTCATTAAAGGTTGTTGATGTG GAGGAGCAACAGCTGGAAGAGTCTGGGCCACACGATTTGAC GGAAACATCTTACTTGCCAAGGCAAGATCTAGGTAATA	925
	TATTACCTAGATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAA ATCGTGTGGCCAGACTCTTCCAGCTGTTGCTCCTCCACATC AACAACTTAATGAGCTCCTCTTGAGATGGGTAGTT	926
	AGCTGGAAGAGTCTGGG	927
	CCCAGACTCTTCCAGCT	928
Breast Cancer Tyr-1563-Stop TAC to TAG	TTTGTAATTCAACATTCATCGTTGTGTAAATTAACTTCTCCCA TTCCTTTCAGAGGGGAACCCCTTACCTGGAATCTGGAATCAGC CTCTTCTCTGATGACCCTGAATCTGATCCTTCTGA	929
	TCAGAAGGATCAGATTCAGGGTCATCAGAGAAGAGGCTGATT CCAGATTCCAGGTAAGGGGTTCCCTCTGAAAGGAATGGGAG AAGTTTAATTTACACAACGATGAATGTTGAATTACAAA	930
	AGAGGGAACCCCTTACC	931
	GGTAAGGGGTTCCCTCT	932
Breast Cancer Leu-1564-Pro CTG to CCG	CAACATTCATCGTTGTGTAAATTAACTTCTCCCATTCCTTTC AGAGGGAACCCCTTACCTGGAATCTGGAATCAGCCTCTTCTC TGATGACCCTGAATCTGATCCTTCTGAAGACAGAGC	933
	GCTCTGTCTTCAGAAGGATCAGATTCAGGGTCATCAGAGAAG AGGCTGATTCCAGATTCCAGGTAAGGGGTTCCCTCTGAAAG GAATGGGAGAAGTTTAATTTACACAACGATGAATGTTG	934

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CCCTTACCTGGAATCTG	935
	CAGATTCCAGGTAAGGG	936
Breast Cancer Gln-1604-Stop CAA to TAA	GCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACC TCTGCATTGAAAGTTCCCAATTGAAAGTTGCAGAATCTGCC CAGAGTCCAGCTGCTGCTCATACTACTGATACTGCTG	937
	CAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCTGGGCA GATTCTGCAACTTTCAATTGGGGAAGTTTCAATGCAGAGGTT GAAGATGGTATGTTGCCAACACGAGCTGACTCTGGGGC	938
	AAGTTCCCAATTGAAA	939
	TTTCAATTGGGGAAGTT	940
Breast Cancer Lys-1606-Glu AAA to GAA	GAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCA TTGAAAGTTCCCAATTGAAAGTTGCAGAATCTGCCAGAGT CCAGCTGCTGCTCATACTACTGATACTGCTGGGTATA	941
	TATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCT GGGCAGATTCTGCAACTTTCAATTGGGGAAGTTTCAATGCAG AGGTTGAAGATGGTATGTTGCCAACACGAGCTGACTC	942
	CCCAATTGAAAGTTGCA	943
	TGCAACTTTCAATTGGG	944
Breast Cancer Met-1628-Thr ATG to ACG	CAGAATCTGCCAGAGTCCAGCTGCTGCTCATACTACTGATA CTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAG AAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACA	945
	TTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCC TGCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGT AGTATGAGCAGCAGCTGGACTCTGGGCAGATTCTG	946
	TAATGCAATGGAAGAAA	947
	TTTCTTCCATTGCATTA	948
Breast Cancer Met-1628-Val ATG to GTG	GCAGAATCTGCCAGAGTCCAGCTGCTGCTCATACTACTGAT ACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGA GAAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACA	949
	TGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCT GCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGTA GTATGAGCAGCAGCTGGACTCTGGGCAGATTCTGC	950
	ATAATGCAATGGAAGAA	951

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO
	TTCTTCCATTGCATTAT	952
Breast Cancer Pro-1637-Leu CCA to CTA	CTCATACTACTGATACTGCTGGGTATAATGCAATGGAAGAAA GTGTGAGCAGGGAGAAGCCAGAATTGACAGCTTCAACAGAA AGGGTCAACAAAAGAATGTCCATGGTGGTGTCTGGCCT	953
	AGGCCAGACACCACCATGGACATTCTTTTGTGACCCTTTCT GTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTCACACTTTCTT CCATTGCATTATACCCAGCAGTATCAGTAGTATGAG	954
	GGAGAAGCCAGAATTGA	955
	TCAATTCTGGCTTCTCC	956
Breast Cancer Met-1652-Ile ATG to ATA	GAGCAGGGAGAAGCCAGAATTGACAGCTTCAACAGAAAGGG TCAACAAAAGAATGTCCATGGTGGTGTCTGGCCTGACCCCAG AAGAATTTGTGAGTGTATCCATATGTATCTCCCTAATG	957
	CATTAGGGAGATACATATGGATACACTCACAAATTCTTCTGG GGTCAGGCCAGACACCACCATGGACATTCTTTTGTGACCCT TTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTC	958
	ATGTCCATGGTGGTGTC	959
	GACACCACCATGGACAT	960
Breast Cancer Glu-1694-Stop GAG to TAG	CACTTCCTGATTTTGTTCCTCAACTTCTAATCCTTTGAGTGTTT TCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGACACTGAA ATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG	961
	CTACCCATTTTCTCCCGCAATTCCTAGAAAATATTTCAAGTGT CCGTTACACACAAACTCAGCATCTGCAGAATGAAAAACACT CAAAGGATTAGAAGTTGAAAACAAAATCAGGAAGTG	962
	CAGATGCTGAGTTTGTG	963
	CACAAACTCAGCATCTG	964
Breast Cancer Gly-1706-Glu GGA to GAA	GTGTTTTTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGA CACTGAAATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG TTAGCTATTTCTGTAAGTATAATACTATTTCTCCCT	965
	AGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACCC ATTTTCTCCCGCAATTCCTAGAAAATATTTCAAGTGTCCGTTT ACACACAAACTCAGCATCTGCAGAATGAAAAACAC	966
	TTTTCTAGGAATTGCGG	967
	CCGCAATTCCTAGAAA	968

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Ala-1708-Glu GCG to GAG	TTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGACACTGA AATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAGTTAGCT ATTTCTGTAAGTATAATACTATTTCTCCCCTCCTCCC	969
	GGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTA ACTACCCATTTTCTCCC <u>G</u> CAATTCCTAGAAAATATTTTCAGTG TCCGTTACACACAAACTCAGCATCTGCAGAATGAA	970
	AGGAATTGCGGGAGGAA	971
	TTCTCCC <u>G</u> CAATTCCT	972
Breast Cancer Val-1713-Ala GTA to GCA	CTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAAT TGCGGGAGGAAAATGGGTAGTTAGCTATTTCTGTAAGTATAA TACTATTTCTCCCCTCCTCCCTTAAACACCTCAGAA	973
	TTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATAC TTACAGAAATAGCTAACTACCCATTTTCTCCC <u>G</u> CAATTCCTA GAAAATATTTTCAGTGTCGTTACACACAAACTCAG	974
	AAAATGGGTAGTTAGCT	975
	AGCTAACTACCCATTTT	976
Breast Cancer Trp-1718-Stop TGG to TAG	AACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAAT GGGTAGTTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCT CCTCCCTTTAAACACCTCAGAATTGCATTTTACACC	977
	GGTGTA AAAATGCAATTCTGAGGTGTTAAAGGGAGGAGGGG AGAAATAGTATTATACTTAGAGAAATAGCTAACTACCCATTTTC CTCCCGCAATTCCTAGAAAATATTTTCAGTGTCGTT	978
	CTATTTCTGTAAGTATA	979
	TATACTTACAGAAATAG	980
Breast Cancer Glu-1725-Stop GAA to TAA	TTCTGCTGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGG TGACCCAGTCTATTAAAGAAAGAAAAATGCTGAATGAGGTAA GTA CTTGATGTTACAACTAACCAGAGATATTCATT	981
	AATGAATATCTCTGGTTAGTTTGTAACATCAAGTACTTACCTC ATTCAGCATTTTCTTTCTTTAATAGACTGGGTCACCCCTAAA GAGATCATAGAAAAGACAGGTTACATACAGCAGAA	982
	CTATTAAAGAAAGAAAA	983
	TTTTCTTTCTTTAATAG	984
Breast Cancer Lys-1727-Stop AAA to TAA	TGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGGTGACCC AGTCTATTAAAGAAAGAAATGCTGAATGAGGTAAGTACTTG ATGTTACAACTAACCAGAGATATTCATTCA GTCA	985

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGACTGAATGAATATCTCTGGTTAGTTTGTAACATCAAGTACT TACCTCATTGAGCATT TT TCTTTCTTTAATAGACTGGGTCACC CCTAAAGAGATCATAGAAAAGACAGGTTACATACA	986
	AAGAAAGAAAATGCTG	987
	CAGCATT TT TCTTTCTT	988
Breast Cancer Pro-1749-Arg CCA to CGA	TCTTTCAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATG GAAGAAACCACCAAGGTCCAAAGCGAGCAAGAGAATCCCAG GACAGAAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAA	939
	TTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGTCCTGG GATTCTCTTGCTCGCTTTGGACCTTGGTGGTTTCTTCCATTGA CCACATCTCCTCTGACTTCAAATCATGCTGAAAGA	990
	CCAAGGTCCAAAGCGAG	991
	CTCGCTTTGGACCTTGG	992
Breast Cancer Arg-1751-Stop CGA to TGA	CAGCATGATTTTGAAGTCAGAGGAGTGTGGTCAATGGAAGA AACCACCAAGGTCCAAAGCGAGCAAGAAGAATCCCAGGACAG AAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAAATCTC	993
	GAGATTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGT CCTGGGATTCTCTTGCTCGCTTTGGACCTTGGTGGTTTCTTC CATTGACCACATCTCCTCTGACTTCAAATCATGCTG	994
	GTCCAAAGCGAGCAAGA	995
	TCTTGCTCGCTTTGGAC	996
Breast Cancer Gln-1756-Stop CAG to TAG	GTCAGAGGAGATGTGGTCAATGGAAGAAACCACCAAGGTCC AAAGCGAGCAAGAGAATCCCAGGACAGAAAGGTAAAGCTCC CTCCCTCAAGTTGACAAAAATCTCACCCACCACTCTGT	997
	ACAGAGTGGTGGGGTGAGATTTTGTCAACTTGAGGGAGGG AGCTTTACCTTTCTGTCCTGGGATTCTCTTGCTCGCTTTGGA CCTTGGTGGTTTCTTCCATTGACCACATCTCCTCTGAC	998
	GAGAATCCCAGGACAGA	999
	TCTGTCCTGGGATTCTC	1000
Breast Cancer Met-1775-Arg ATG to AGG	CTCTCTTCTTCCAGATCTTCAGGGGGCTAGAAATCTGTTGCT ATGGGCCCTTACCAACATGCCACAGGTAAGAGCCTGGGA GAACCCAGAGTTCCAGCACCAGCCTTTGTCTTACATA	1001
	TATGTAAGACAAAGGCTGGTGGTGGAACTCTGGGGTTCTCCC AGGCTCTTACCTGTGGGCATGTTGGTGAAGGGCCCATAGCA ACAGATTTCTAGCCCCCTGAAGATCTGGAAGAAGAGAG	1002

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CACCAACATGCCACAG	1003
	CTGTGGGCATGTTGGTG	1004
Breast Cancer Trp-1782-Stop TGG to TGA	AGTATGCAGATTACTGCAGTGATTTTACATCTAAATGTCCATT TTAGATCAACTGGAATGGATGGTACAGCTGTGTGGTGCTTCT GTGGTGAAGGAGCTTTCATCATTACCCTTGGCACA	1005
	TGTGCCAAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGC ACCACACAGCTGTACCATCCATTCCAGTTGATCTAAAATGGA CATTTAGATGTAAAATCACTGCAGTAATCTGCATACT	1006
	CTGGAATGGATGGTACA	1007
	TGTACCATCCATTCCAG	1008
Breast Cancer Gln-1785-His CAG to CAT	ATTACTGCAGTGATTTTACATCTAAATGTCCATTTTAGATCAAC TGGAATGGATGGTACAGCTGTGTGGTGCTTCTGTGGTGAAG GAGCTTTCATCATTACCCTTGGCACAGTAAGTATT	1009
	AATACTTACTGTGCCAAGGGTGAATGATGAAAGCTCCTTCAC CACAGAAGCACCACACAGCTGTACCATCCATTCCAGTTGATC TAAAATGGACATTTAGATGTAAAATCACTGCAGTAAT	1010
	ATGGTACAGCTGTGTGG	1011
	CCACACAGCTGTACCAT	1012
Breast Cancer Glu-1794-Asp GAG to GAT	GTCCATTTTAGATCAACTGGAATGGATGGTACAGCTGTGTGG TGCTTCTGTGGTGAAGGAGCTTTCATCATTACCCTTGGCAC AGTAAGTATTGGGTGCCCTGTCAGAGAGGGAGGACAC	1013
	GTGTCCTCCCTCTCTGACAGGGCACCCAATACTTACTGTGCC AAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGCACCACA CAGCTGTACCATCCATTCCAGTTGATCTAAAATGGAC	1014
	GTGAAGGAGCTTTCATC	1015
	GATGAAAGCTCCTTCAC	1016
Breast Cancer Arg-1835-Stop CGA to TGA	CTCTGCTTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGT GAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGT AGCACTCTACCAGTGCCAGGAGCTGGACACCTACCTGA	1017
	TCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACA CTGTCCAACACCCACTCTCGGGTCACCACAGGTGCCTCACA CATCTGCCCAATTGCTGGAGACAGAGAACAACAAGCAGAG	1018
	TGGTGACCCGAGAGTGG	1019
	CCACTCTCGGGTCACCA	1020

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Trp-1837-Arg TGG to CGG	TTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCA CCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGTAGCACT CTACCAGTGCCAGGAGCTGGACACCTACCTGATACCCC	1021
	GGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGT GCTACACTGTCCAACACCCACTCTCGGGTCACCACAGGTGC CTCACACATCTGCCCAATTGCTGGAGACAGAGAACACAA	1022
	CCCGAGAGTGGGTGTTG	1023
	CAACACCCACTCTCGGG	1024
Breast Cancer Trp-1837-Stop TGG to TAG	TGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCAC CTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGTAGCACTC TACCAGTGCCAGGAGCTGGACACCTACCTGATACCCCA	1025
	TGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAG TGCTACACTGTCCAACACCCACTCTCGGGTCACCACAGGTG CCTCACACATCTGCCCAATTGCTGGAGACAGAGAACACA	1026
	CCGAGAGTGGGTGTTGG	1027
	CCAACACCCACTCTCGG	1 3

Table 15
BRCA2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer PHE32LEU TTT to CTT	GTAAACTAAGGTGGGATTTTTTTTAAATAGATTTAGGAC CAATAAGTCTTAATTGGTTGAAGAACTTTCTTCAGAAGCTCC ACCCTATAATTCTGAACCTGCAGAAGAATCTGAAC	1029
	GTTCAGATTCTTCTGCAGGTTTCAAGATTATAGGGTGGAGCTT CTGAAGAAAGTTCTTCAAACCAATTAAGACTTATTGGTCCTAA ATCTATTTAAAAAAAATCCACCTTAGTTTAAAC	1030
	TTAATTGGTTTGAAGAA	1031
	TTCTTCAAACCAATTAA	1032
Breast cancer TYR42CYS TAT to TGT	TAGATTTAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTC TTCAGAAGCTCCACCCTATAATTCTGAACCTGCAGAAGAATC TGAACATAAAAACAACAATTACGAACCAACCTATT	1033

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AATAGGTTTGGTTCGTAATTGTTGTTTTATGTTTCAGATTCTTC TGCAGGTTCAGAATTATAGGGTGGAGCTTCTGAAGAAAGTTC TTCAAACCAATTAAGACTTATTGGTCCTAAATCTA	1034
	TCCACCCTATAATTCTG	1035
	CAGAATTATAGGGTGGGA	1036
Breast cancer LYS53ARG AAA to AGA	AAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC AGAAGAATCTGAACATAAAACAACAATTACGAACCAAACCTA TTTAAACTCCACAAAGGAAACCATCTTATAATCA	1037
	TGATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAGGTTTG GTTTCGTAATTGTTGTTTTATGTTTCAGATTCTTCTGCAGGTTT AGAATTATAGGGTGGAGCTTCTGAAGAAAGTTCTT	1038
	TGAACATAAAACAACA	1039
	TGTTGTTTTTATGTTCA	1040
Breast cancer Phe81Leu TTC to CTC	CTATTTAAACTCCACAAAGGAAACCATCTTATAATCAGCTGG CTTCAACTCCAATAATATTCAAAGAGCAAGGGCTGACTCTGC CGCTGTACCAATCTCCTGTAAAGAATTAGATAAAT	1041
	ATTTATCTAATTCTTTTACAGGAGATTGGTACAGCGGCAGAGT CAGCCCTTGCTCTTTGAATATTATTGGAGTTGAAGCCAGCTG ATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAG	1042
	CAATAATATTCAAAGAG	1043
	CTCTTTGAATATTATTG	1044
Breast cancer TRP194TERM TGG to TAG	GTCAGACACCAAACATATTTCTGAAAGTCTAGGAGCTGAGG TGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACC CACCTTAGTTCTACTGTGCTCATAGGTAATAATAG	1045
	CTATTATTACCTATGAGCACAGTAGAACTAAGGGTGGGTGGT GTAGCTAAAGAACTTGACCAAGACATATCAGGATCCACCTCA GCTCCTAGACTTTCAGAAATATGTTTTGGTGTCTGAC	1046
	TATGTCTTGGTCAAGTT	1047
	AACTTGACCAAGACATA	1048
Breast cancer PRO201ARG CCA to CGA	CTGAAAGTCTAGGAGCTGAGGTGGATCCTGATATGTCTTGGT CAAGTTCTTTAGCTACACCACCCACCCTTAGTTCTACTGTGCT CATAGGTAATAATAGCAAATGTGTATTTACAAGAAA	1049
	TTTCTTGTAATACACATTTGCTATTATTACCTATGAGCACAGT AGAATAAGGGTGGGTGGTGTAGCTAAAGAACTTGACCAAGA CATATCAGGATCCACCTCAGCTCCTAGACTTTCAG	1050

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGCTACACCACCCACCC	1051
	GGGTGGGTGGTGTAGCT	1052
Breast cancer Pro222Ser CCT to TCT	ACAATACACATAAATTTTATCTTACAGTCAGAAATGAAGAAG CATCTGAAACTGTATTTCTCATGATACTACTGCTGTAAGTAA ATATGACATTGATTAGACTGTTGAAATTGCTAACA	1053
	TGTTAGCAATTTCAACAGTCTAATCAATGTCATATTTACTTACA GCAGTAGTATCATGAGGAAATACAGTTTCAGATGCTTCTTCAT TTCTGACTGTAAGATAAAAATTTATGTGTATTGT	1054
	CTGTATTTCTCATGAT	1055
	ATCATGAGGAAATACAG	1056
Breast cancer Leu-414-Term TTG to TAG	AATGGTCTCAACTAACCCTTTCAGGTCTAAATGGAGCCCAGA TGGAGAAAATACCCCTATTGCATATTTCTTCATGTGACCAAAA TATTTAGAAAAAGACCTATTAGACACAGAGAACAA	1057
	TTGTTCTCTGTGTCTAATAGGTCTTTTCTGAAATATTTTGGTC ACATGAAGAAATATGCAATAGGGGTATTTTCTCCATCTGGGC TCCATTTAGACCTGAAAGGGTTAGTTGAGACCATT	1058
	ACCCCTATTGCATATTT	1059
	AAATATGCAATAGGGGT	1060
Breast cancer, male Cys554Trp TGT to TGG	AGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACA GAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAG CTGGCCAGCCACCACCACAGAAATTCTGTAGCTTTG	1061
	CAAAGCTACAGAATTCTGTGTGGTGGTGGCTGGCCAGCTTC CATTATCAATTAATTTGGACATAAGGAGTCCTCCTTCTGTGA GCAAACAGTATGTATTTCCAGTCCACTTTCAGAGGCT	1062
	TCCTTATGTCCAAATTT	1063
	AAATTTGGACATAAGGA	1064
Breast cancer Lys944Term AAA to TAA	AACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAA GCAACCCAAGTGTCAATTAAAAAGATTTGGTTTTATGTTCTTG CAGAGGAGAACAAAAATAGTGTAAGCAGCATATAA	1065
	TTATATGCTGCTTTACACTATTTTGTTCCTCTGCAAGAAC ATAAACCAAATCTTTTTAATTGACACTTGGGTGCTTGTTTAT CACCTGTGTCTCCATATAAAACCATGGTAGAGTT	1066
	TGTCAATTAAAAAGAT	1067
	ATCTTTTTTAATTGACA	1068

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Breast cancer, male Glu1320Term GAA to TAA	ATGACTACTGGCACTTTTGTGGAAGAAATTACTGAAAATTACA AGAGAAATACTGAAAATGAAGATAACAAATATACTGCTGCCAG TAGAAATTCTCATAACTTAGAATTTGATGGCAGTG	1069
	CACTGCCATCAAATTCTAAGTTATGAGAATTTCTACTGGCAGC AGTATATTTGTTATCTTCATTTTCAGTATTTCTCTTGTAATTTTC AGTAATTTCTTCAACAAAAGTGCCAGTAGTCAT	1070
	CTGAAAATGAAGATAAC	1071
	GTTATCTTCATTTTCAG	1072
Breast cancer Glu1876Term GAA to TAA	CATGAAACAATTAAGGAGACATATTTACAGACAGTT TCAGTAAAGTAATTAAGGAAAACAACGAGAATAAATCAAAAAT TTGCCAAACGAAAATTATGGCAGGTTGTTACGAGG	1073
	CCTCGTAACAACCTGCCATAATTTTCGTTTGGCAAATTTTGA TTTATTCTCGTTGTTTTCTTAATTACTTTACTGAAACTGTCTG TAAATATGTCTTTCACTTTTTAATTGTTTCATG	1074
	TAATTAAGGAAAACAAC	1075
	GTTGTTTTCTTAATTA	1076
Breast cancer Ser1882Term TCA to TAA	TGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAGGA AAACAACGAGAATAAATCAAAAATTTGCCAAACGAAAATTATG GCAGGTTGTTACGAGGCATTGGATGATTCAGAGGA	1077
	TCCTCTGAATCATCCAATGCCTCGTAACAACCTGCCATAATTT TCGTTTGGCAAATTTTGAATTTATTCTCGTTGTTTTCTTAATT ACTTTACTGAAACTGTCTGTAAATATGTCTTTCA	1078
	GAATAAATCAAAAATTT	1079
	AAATTTTGAATTTATTC	1080
Breast cancer Glu1953Term GAA to TAA	AACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAAATATCAC CTTGTGATGTTAGTTTGGAACTTCAGATATATGTAAATGTAG TATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAA	1081
	TTGCAGATGAGACTGACTTATGAAGCTTCCCTATACTACATTT ACATATATCTGAAGTTTCCAACTAACATCACAAGGTGATATT TTAGAACTTTCTCCAATCCAGACATATTTTGGTT	1082
	TTAGTTTGGAACTTCA	1083
	TGAAGTTTCCAACTAA	1084
Breast cancer Ser1970Term TCA to TAA	TTAGTTTGGAACTTCAGATATATGTAAATGTAGTATAGGGAA GCTTCATAAGTCAGTCTCATCTGCAAATACTTGTGGGATTTT AGCACAGCAAGTGGAATCTGTCCAGGTATCAGA	1085

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGATACCTGGACAGATTTTCCACTTGCTGTGCTAAAATCC CACAAGTATTTGCAGATGAGACTGACTTATGAAGCTTCCCTAT ACTACATTTACATATATCTGAAGTTTCCAACTAA	1086
	GTCAGTCTCATCTGCAA	1087
	TTGCAGATGAGACTGAC	1088
Breast cancer Gln1987Term CAG to TAG	AAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTATGCACAG CAAGTGGAAAATCTGTCCAGGTATCAGATGCTTCATTACAAAA CGCAAGACAAGTGTTTTCTGAAATAGAAGATAGTA	1089
	TACTATCTTCTATTTAGAAAACACTTGTCTTGCCTTTTGTAA GAAGCATCTGATACCTGGACAGATTTTCCACTTGCTGTGCTA AAAATCCCACAAGTATTTGCAGATGAGACTGACTT	1090
	AATCTGTCCAGGTATCA	1091
	TGATACCTGGACAGATT	1092
Breast cancer Ala2466Val GCA to GTA	AAAATAAGATTAATGACAATGAGATTCATCAGTTTAACAAAA CAACTCCAATCAAGCAGCAGCTGTAACCTTCACAAAGTGTGA AGAAGAACCTTTAGGTATTGTATGACAATTTGTGTG	1093
	CACACAAATTGTCATACAATACCTAAAGGTTCTTCTTCACACT TTGTGAAAGTTACAGCTGCTGCTTGATTGGAGTTGTTTTGTT AAACTGATGAATCTCATTGTCATTAATCTTATTTT	1094
	TCAAGCAGCAGCTGTAA	1095
	TTACAGCTGCTGCTTGA	1096
Breast cancer Arg2520Term CGA to TGA	AGGCAACGCGTCTTTCCACAGCCAGGCAGTCTGTATCTTGCA AAACATCCACTCTGCCTCGAATCTCTCTGAAAGCAGCAGTA GGAGGCCAAGTCCCCTCTGCGTGCTCATAAACAGG	1097
	CCTGTTTATGAGGACACGCAGAGGGGACTTGGCCTCCTACT GCTGCTTTCAGAGAGATTCCAGGCAGAGTGGATGTTTTTGCA AGATACAGACTGCCTGGCTGTGGAAAGACGCGTTGCCT	1098
	CTCTGCCTCGAATCTCT	1099
	AGAGATTCGAGGCAGAG	1100
Breast cancer Gln2714Term CAA to TAA	ATTTCAATTGAGCGCAAATATATCTGAACTTCTAGCAATAAAA CTAGTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTA CAGATGGGTGGTATGCTGTAAAGGCCAGTTAGATC	1101
	GATCTAACTGGGCCTTAACAGCATACCACCCATCTGTAAGTT CAATAATGGCCACTTTTTGGGTATCTGCACTACTAGTTTTATT GCTAGAAGTTTCAGATATATTTGCGCTCAATGAAAT	1102

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGATACCC <u>AAAA</u> AGTG	1103
	CACTTTTTGGGTATCTG	1104
Breast cancer Leu2776Term TTA to TGA	CAGAACTGGTGGGCTCTCCTGATGCCTGTACACCTCTTGAAG CCCCAGAATCTCTTATGTTAAAGGTAAATTAATTTGCACTCTT GGTAAAAATCAGTCATTGATTGAGTTAAATTCTAGA	1105
	TCTAGAATTTAACTGAATCAATGACTGATTTTTACCAAGAGTG CAAATTAATTTACCTTTAACATAAGAGATTCTGGGGCTTCAAG AGGTGTACAGGCATCAGGAGAGCCCACCAGTTCTG	1106
	TCTTATGTTAAAGATTT	1107
	AAATCTTTAACATAAGA	1108
Breast cancer Gln2893Term CAG to TAG	CCTTTTGTCTTCTTAGAAAACACAACAAACCATATTTACCATC ACGTGCACTAACAAGAGAGCAAGTTCGTGCTTTGCAAGATGG TGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAG	1109
	CTGCTGCATTCTTCACTGCTTCATAAAGCTCTGCACCATCTTG CAAAGCACGAACCTTGCTGTCTTGTTAGTGACGTGATGGTAA ATATGGTTTTGTTGTGTTTTCTAAGAAAACAAAAGG	1110
	TAACAAGAGAGCAAGTT	1111
	AACTTGCTGTCTTGTTA	1112
Breast cancer Ala2951Thr GCC to ACC	AATCACAGGCCAATGTTGAATGATAAGAAACAAGCTCAGATC CAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAG GAACAAGGTTTATCAAGGGATGTCACAACCGTGTGGA	1113
	TCCACACGGTTGTGACATCCCTTGATAAACCTTGTTCTTTTG TTCAGCAGATTCATGGCCTTCCTAATTTCCAACCTGGATCTGA GCTTGTTTCTTATCATTCAACATTTGCCTGTGATT	1114
	TTAGGAAGGCCATGGAA	1115
	TTCCATGGCCTTCCTAA	1116
Breast cancer Met3118Thr ATG to ACG	ACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGA CATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAG TGGCGACCAGAATCCAAATCAGGCCTTCTTACTTT	1117
	AAAGTAAGAAGGCCTGATTTGGATTCTGGTCGCCACTGGAG GTTGCTTGCAAGCAATTAACATATGAGGCTTAATAATGTCCTCA TTAAGGTCTATCCAAAACCTTATTGCCAGTAAATTGT	1118
	GCCTCATATGTTAATTG	1119
	CAATTAACATATGAGGC	1120

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer Thr3401Met ACG to ATG	GACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGG AGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGC AGGACACAATTACAACATAAAAAATATATCTAAGCATT	1121
	AATGCTTAGATATATTTTTTAGTTGTAATTGTGTCCTGCTTATT TTTCTCACATTCTTCCGTACTGGCCTGGGAACCTCTCCTGTTCT TTGATCAGAGATGTAGTACAACGTCGTTTCAGTC	1122
	GGCCAGTACGGAAGAAT	1123
	ATTCTTCCGTACTGGCC	1124
Breast cancer Ile3412Val ATT to GTT	AAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGA GAAAAATAAGCAGGACACAATTACAACATAAAAAATATATCTAA GCATTTGCAAAGGCGACAATAAATTATTGACGCTTAA	1125
	TTAAGCGTCAATAATTTATTGTGCGCCTTTGCAAATGCTTAGAT ATATTTTTTAGTTGTAATTGTGTCCTGCTTATTTTTCTCACATT CTTCCGTACTGGCCTGGGAACCTCTCCTGTTCTTT	1126
	AGGACACAATTACAAC	1127
	AGTTGTAATTGTGTCCT	1128

EXAMPLE 9

Cystic Fibrosis - CFTR

Cystic fibrosis is a lethal disease affecting approximately one in 2,500 live Caucasian births and is the most common autosomal recessive disease in Caucasians. Patients with this disease have reduced chloride ion permeability in the secretory and absorptive cells of organs with epithelial cell linings, including the airways, pancreas, intestine, sweat glands and male genital tract. This, in turn, reduces the transport of water across the epithelia. The lungs and the GI tract are the predominant organ systems affected in this disease and the pathology is characterized by blocking of the respiratory and GI tracts with viscous mucus. The chloride impermeability in affected tissues is due to mutations in a specific chloride channel, the cystic fibrosis transmembrane conductance regulator protein (CFTR), which prevents normal passage of chloride ions through the cell membrane (Welsh et al., Neuron, 8:821-829 (1992)). Damage to the lungs due to mucus blockage, frequent bacterial infections and inflammation is the primary cause of morbidity and mortality in CF patients and, although maintenance therapy has improved the quality of patients' lives, the median age at death is still only around 30 years. There is no effective treatment for the disease, and therapeutic research is focused on gene therapy using

exogenous transgenes in viral vectors and/or activating the defective or other chloride channels in the cell membrane to normalize chloride permeability (Tizzano et al., J. Pediat., 120:337-349 (1992)). However, the death of a teenage patient treated with an adenovirus vector carrying an exogenous CFTR gene in clinical trials in the late 1990's has impacted this area of research.

The oligonucleotides of the invention for correction of the CFTR gene are attached as a table.

Table 16
CFTR Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Cystic fibrosis Ala46Asp GCT to GAT	AAGGATACAGACAGCGCCTGGAATTGTCAGACATATACCAA TCCCTTCTGTTGATTCTGCTGACAATCTATCTGAAAAATTGGA AAGGTATGTTTCATGTACATTGTTTAGTTGAAGAGAG	1129
	CTCTCTTCAACTAAACAATGTACATGAACATACCTTTCCAATTT TTCAGATAGATTGTCAGCAGAATCAACAGAAGGGATTGGTA TATGTCTGACAATTCCAGGCGCTGTCTGTATCCTT	1130
	TGATTCTGCTGACAATC	1131
	GATTGTCAGCAGAATCA	1132
Cystic fibrosis Ser50Tyr TCT to TAT	AGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTG ATTCTGCTGACAATCTATCTGAAAAATTGGAAAGGTATGTTCA TGACATTGTTTAGTTGAAGAGAGAAATTCATATTA	1133
	TAATATGAATTTCTCTCTTCAACTAAACAATGTACATGAACATA CCTTTCCAATTTTTCAGATAGATTGTCAGCAGAATCAACAGAA GGGATTGGTATATGTCTGACAATTCCAGGCGCT	1134
	CAATCTATCTGAAAAAT	1135
	ATTTTTCAGATAGATTG	1136
Congenital absence of vas deferens Glu56Lys GAA-AAA	AGGACAACTAAAATATTTGCACATGCAACTTATTGGTCCCACT TTTTATTCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAA GAAAAATCCTAACTCATTATGCCCTTCGGCGAT	1137
	ATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTCTTTGAAGC CAGCTCTCTATCCCATTTCTCTGCAAAAGAATAAAAAGTGGGA CCAATAAGTTGCATGTGCAATATTTTAGTTGTCCT	1138
	TTTGCAGAGAATGGGAT	1139
	ATCCCATTTCTCTGCAA	1140

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Trp57Gly TGG to GGG	AGGACAACCTAAAATATTTGCACATGCAACTTATTGGTCCCACT TTTTATTCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAA GAAAAATCCTAACTCATTAAATGCCCTTCGGCGAT	1141
	ATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTCTTTGAAGC CAGCTCTCTATCCCATTTCTCTGCAAAGAATAAAAAGTGGGA CCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT	1142
	TTTGCAGAGAATGGGAT	1143
	ATCCCATTTCTCTGCAA	1144
Cystic fibrosis Trp57Term TGG to TGA	AACTAAAATATTTGCACATGCAACTTATTGGTCCCACTTTTTAT TCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAA ATCCTAACTCATTAAATGCCCTTCGGCGATGTTTT	1145
	AAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTCTTT GAAGCCAGCTCTCTATCCCATTTCTCTGCAAAGAATAAAAAGT GGGACCAATAAGTTGCATGTGCAAATATTTTAGTT	1146
	AGAGAATGGGATAGAGA	1147
	TCTCTATCCCATTTCTCT	1148
Congenital absence of vas deferens Asp58Asn GAT to AAT	ACTAAAATATTTGCACATGCAACTTATTGGTCCCACTTTTTATT CTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAA TCCTAACTCATTAAATGCCCTTCGGCGATGTTTT	1149
	AAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTCTTT TGAAGCCAGCTCTCTATCCCATTTCTCTGCAAAGAATAAAAAG TGGGACCAATAAGTTGCATGTGCAAATATTTTAGT	1150
	GAGAATGGGATAGAGAG	1151
	CTCTCTATCCCATTTCTC	1152
Cystic fibrosis Glu60Term GAG to TAG	ATATTTGCACATGCAACTTATTGGTCCCACTTTTTATTCTTTTG CAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAA ACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGA	1153
	TCCAGAAAAACATCGCCGAAGGGCATTAAATGAGTTTAGGAT TTTTCTTTGAAGCCAGCTCTCTATCCCATTTCTCTGCAAAGAA TAAAAGTGGGACCAATAAGTTGCATGTGCAAATAT	1154
	GGGATAGAGAGCTGGCT	1155
	AGCCAGCTCTCTATCCC	1156

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Pro67Leu CCT to CTT	GGTCCCACTTTTTATTCTTTTGCAGAGAATGGGATAGAGAGC TGGCTTCAAAGAAAAATCCTAACTCATTAAATGCCCTTCGGC GATGTTTTTCTGGAGATTATGTTCTATGGAATCTT	1157
	AAGATTCCATAGAACATAAATCTCCAGAAAAACATCGCCGAA GGGCATTAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTCT ATCCATTCTCTGCAAAAGAATAAAAAGTGGGACC	1158
	GAAAAATCCTAACTCA	1159
	TGAGTTTAGGATTTTTC	1160
Cystic fibrosis Arg74Trp CGG to TGG	TGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCT AACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTTA TGTTCTATGGAATCTTTTTATATTAGGGGTAAGGA	1161
	TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATT TTTCTTTGAAGCCAGCTCTCTATCCATTCTCTGCA	1162
	ATGCCCTTCGGCGATGT	1163
	ACATCGCCGAAGGGCAT	1164
Congenital absence of vas deferens ARG75GLN CGA to CAA	GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTATGTT CTATGGAATCTTTTTATATTAGGGGTAAGGATCTC	1165
	GAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACATCGCCGAAGGGCATTAAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCATTCTC	1166
	CCTTCGGCGATGTTTTT	1167
	AAAAACATCGCCGAAGG	1168
Cystic fibrosis Arg75Leu CGA to CTA	GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTATGTT CTATGGAATCTTTTTATATTAGGGGTAAGGATCTC	1169
	GAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACATCGCCGAAGGGCATTAAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCATTCTC	1170
	CCTTCGGCGATGTTTTT	1171
	AAAAACATCGCCGAAGG	1172
Cystic fibrosis Arg75Term CGA to TGA	AGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAA CTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTATGT TCTATGGAATCTTTTTATATTAGGGGTAAGGATCT	1173

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAA TCTCCAGAAAAACATCGCCGAAGGGCATTAAATGAGTTTAGG ATTTTCTTTGAAGCCAGCTCTCTATCCCATTCTCT	1174
	CCCTTCGGCGATGTTTT	1175
	AAAACATCGCCGAAGGG	1176
Cystic fibrosis Gly85Glu GGA to GAA	AAAATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTTTTCTG GAGATTTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT	1177
	AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAA ACATCGCCGAAGGGCATTAAATGAGTTTAGGATTT	1178
	GTTCTATGGAATCTTT	1179
	AAAAGATTCCATAGAAC	1180
Cystic fibrosis Gly85Val GGA to GTA	AAAATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTTTTCTG GAGATTTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT	1181
	AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAA ACATCGCCGAAGGGCATTAAATGAGTTTAGGATTT	1182
	GTTCTATGGAATCTTT	1183
	AAAAGATTCCATAGAAC	1184
Cystic fibrosis Leu88Ser TTA to TCA	AACTCATTAAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT	1185
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT	1186
	AATCTTTTATATTTAG	1187
	CTAAATATAAAAAGATT	1188
Cystic fibrosis Phe87Leu TTT to CTT	CCTAAACTCATTAAATGCCCTTCGGCGATGTTTTTTCTGGAGAT TTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTC ATTTGTACATTCATTATGTATCACATAACTATATG	1189
	CATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCT TACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAG AAAAACATCGCCGAAGGGCATTAAATGAGTTTAGG	1190

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGGAATCTTTTATAT	1191
	ATATAAAAAGATTCCAT	1192
Cystic fibrosis Leu88Term TTA to TGA	AACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATT GTACATTCATTATGTATCACATAACTATATGCATT	1193
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT	1194
	AATCTTTTATATTTAG	1195
	CTAAATATAAAAAGATT	1196
Cystic fibrosis Leu88Term TTA to TAA	AACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATT GTACATTCATTATGTATCACATAACTATATGCATT	1197
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT	1198
	AATCTTTTATATTTAG	1199
	CTAAATATAAAAAGATT	1200
Cystic fibrosis Gly91Arg GGG to AGG	AATGCCCTTCGGCGATGTTTTTCTGGAGATTATGTTCTATG GAATCTTTTATATTTAGGGGTAAGGATCTCATTGTACATTC ATTATGTATCACATAACTATATGCATTTTGTGAT	1201
	ATCACAAAATGCATATAGTTATGTGATACATAATGAATGTAC AAATGAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAAC ATAAATCTCCAGAAAAACATCGCCGAAGGGCATT	1202
	TATATTTAGGGGTAAGG	1203
	CCTTACCCCTAAATATA	1204
Cystic fibrosis Gln98Arg CAG to CGG	AATAAATGAAATTTAATTTCTCTGTTTTCCCTTTTGTAGGAA GTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATA GCTTCCTATGACCCGGATAACAAGGAGGAACGCTC	1205
	GAGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATT CTTCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTAC AAAAGGGGAAAAACAGAGAAATTAATTTCAATTTATT	1206
	AGCAGTACAGCCTCTCT	1207
	AGAGAGGCTGTACTGCT	1208

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Gln98Term CAG-TAG	AAATAAATGAAATTTAATTTCTCTGTTTTTCCCCTTTTGTAGGA AGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCAT AGCTTCCTATGACCCGGATAACAAGGAGGAACGCT	1209
	AGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTC TTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACA AAAGGGGAAAAACAGAGAAATTAATTTTCATTTATT	1210
	AAGCAGTACAGCCTCTC	1211
	GAGAGGCTGTACTGCTT	1212
Cystic fibrosis Ser108Phe TCC to TTC	CCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTAC TGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGG AACGCTCTATCGCGATTTATCTAGGCATAGGCTTATG	1213
	CATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCC TTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAG AGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGG	1214
	CATAGCTTCCTATGACC	1215
	GGTCATAGGAAGCTATG	1216
Cystic fibrosis Tyr109Cys TAT to TGT	TTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGG GAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAAC GCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCT	1217
	AGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCC TCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGT AAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAA	1218
	AGCTTCCTATGACCCGG	1219
	CCGGGTCATAGGAAGCT	1220
Cystic fibrosis Asp110His GAC to CAC	TTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGA AGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGC TCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTC	1221
	GAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTT CCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCA GTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAA	1222
	CTTCCTATGACCCGGAT	1223
	ATCCGGGTCATAGGAAG	1224

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Congenital absence of vas deferens Pro111Leu CCG to CTG	AGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAA TCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTA TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTT	1225
	AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAG CGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTT CCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCT	1226
	CTATGACCCGGATAACA	1227
	TGTTATCCGGGTCATAG	1228
Cystic fibrosis Arg117Cys CGC to TGC	GTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGAC CCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGC ATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGC	1229
	GCAGTGTCTCACATAAAGAGAAGGCATAAGCCTATGCCTA GATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGTCAT AGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTAC	1230
	AGGAGGAACGCTCTATC	1231
	GATAGAGCGTTCCTCCT	1232
Cystic fibrosis Arg117His CGC to CAC	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1233
	AGCAGTGTCTCACATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGTCA TAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTA	1234
	GGAGGAACGCTCTATCG	1235
	CGATAGAGCGTTCCTCC	1236
Cystic fibrosis Arg117Leu CGC to CTC	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1237
	AGCAGTGTCTCACATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGTCA TAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTA	1238
	GGAGGAACGCTCTATCG	1239
	CGATAGAGCGTTCCTCC	1240

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Arg117Pro CGC to CCC	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAAC <u>G</u> CTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1241
	AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAG <u>C</u> GTTCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA	1242
	GGAGGAAC <u>G</u> CTCTATCG	1243
	CGATAGAG <u>C</u> GTTCTCC	1244
Cystic fibrosis Ala120Thr GCG-ACG	CTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAAC AAGGAGGAACGCTCTATC <u>G</u> CGATTTATCTAGGCATAGGCTTA TGCCTTCTCTTTATTGTGAGGACACTGCTCCTACACC	1245
	GGTGTAGGAGCAGTGTCTCACAATAAAGAGAAGGCATAAG CCTATGCCTAGATAAATCG <u>C</u> GATAGAGCGTTCTCCTTGTTA TCCGGGTCATAGGAAGCTATGATTCTTCCAGTAAGAG	1246
	GCTCTATC <u>G</u> CGATTTAT	1247
	ATAAATCG <u>C</u> GATAGAGC	1248
Cystic fibrosis Tyr122Term TAT to TAA	GGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGA ACGCTCTATCGCGATTTAT <u>T</u> CTAGGCATAGGCTTATGCCTTCT CTTTATTGTGAGGACACTGCTCCTACACCCAGCCATT	1249
	AATGGCTGGGTGTAGGAGCAGTGTCTCACAATAAAGAGAA GGCATAA <u>T</u> CCTATGCCTAGATAAATCGCGATAGAGCGTTCT CCTTGTT/ <u>C</u> CGGGTCATAGGAAGCTATGATTCTTCCC	1250
	GCGATTTAT <u>T</u> CTAGGCAT	1251
	ATGCCTAG <u>A</u> TAAATCGC	1252
Cystic fibrosis Gly126Asp GGC-GAC	TAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCG CGATTTATCTAGGCATAG <u>G</u> CTTATGCCTTCTCTTTATTGTGAG GACACTGCTCCTACACCCAGCCATTTTGGCCTTCA	1253
	TGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTCAC AATAAAGAGAAGGCATAAG <u>C</u> CTATGCCTAGATAAATCGCGAT AGAGCGTTCTCCTTGTTATCCGGGTCATAGGAAGCTA	1254
	AGGCATAG <u>G</u> CTTATGCC	1255
	GGCATAAG <u>C</u> CTATGCCT	1256

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis His139Arg CAC to CGC	TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGT GAGGACACTGCTCCTAC <u>AC</u> CCAGCCATTTTTGGCCTTCATCA CATTGGAATGCAGATGAGAATAGCTATGTTTAGTTT	1257
	AAACTAAACATAGCTATTCTCATCTGCATTCCAATGTGATGAA GGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTCACAATA AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGA	1258
	GCTCCTAC <u>AC</u> CCAGCCA	1259
	TGGCTGGGTGTAGGAGC	1260
Cystic fibrosis Ala141Asp GCC to GAC	TTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGAC ACTGCTCCTACACCCAG <u>CC</u> ATTTTTGGCCTTCATCACATTGG AATGCAGATGAGAATAGCTATGTTTAGTTTGATTGA	1261
	TAAATCAAACAACTAAACATAGCTATTCTCATCTGCATTCCAATGT GATGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTC ACAATAAAGAGAAGGCATAAGCCTATGCCTAGATAAA	1262
	ACACCCAG <u>CC</u> ATTTTTG	1263
	CAAAAATGGCTGGGTGT	1264
Cystic fibrosis Ile148Thr ATT to ACT	GCCTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCA TTTTTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTAT GTTTAGTTTGATTATAAGAAGGTAATACTTCCTTG	1265
	CAAGGAAGTATTACCTTCTTATAAATCAAACAACTAAACATAGCTA TTCTCATCTGCATTCCAATGTGATGAAGGCCAAAAATGGCTG GGTGTAGGAGCAGTGTCTCACAATAAAGAGAAGGC	1266
	TCATCACATTGGAATGC	1267
	GCATTCCAATGTGATGA	1268
Cystic fibrosis Gly149Arg GGA to AGA	CTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCATTT TTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTATGTT TAGTTTGATTATAAGAAGGTAATACTTCCTTGCA	1269
	TGCAAGGAAGTATTACCTTCTTATAAATCAAACAACTAAACATAGC TATTCTCATCTGCATTCCAATGTGATGAAGGCCAAAAATGGCT GGGTGTAGGAGCAGTGTCTCACAATAAAGAGAAG	1270
	ATCACATTGGAATGCAG	1271
	CTGCATTCCAATGTGAT	1272

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Gln151Term CAG to TAG	TTTATTGTGAGGACACTGCTCCTACACCCAGCCATTTTGGC CTTCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGTT TGATTTATAAGAAGGTAATACTTCCTTGACACAGGCC	1273
	GGCCTGTGCAAGGAAGTATTACCTTCTTATAAATCAAATAAA CATAGCTATTCTCATCTGCATTCCAATGTGATGAAGGCCAAAA ATGGCTGGGTGTAGGAGCAGTGTCTCACAATAAA	1274
	TTGGAATGCAGATGAGA	1275
	TCTCATCTGCATTCCAA	1276
Cystic fibrosis Lys166Glu AAG-GAG	AATATATTTGTATTTTGTGTTGAAATTATCTAACTTTCCATTT TTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCTAGATAAAA TAAGTATTGGACAACCTGTTAGTCTCCTTTCCA	1277
	TGGAAAGGAGACTAACAAGTTGTCCAATACTTATTTTATCTAG AACACGGCTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA GTTAGATAATTTCAACAAACAAAATACAAATATATT	1278
	AGACTTTAAAGCTGTCA	1279
	TGACAGCTTTAAAGTCT	1280
Cystic fibrosis Ile175Val ATA-GTA	TTATCTAACTTTCCATTTTCTTTTAGACTTTAAAGCTGTCAAG CCGTGTTCTAGATAAAAATAAGTATTGGACAACCTGTTAGTCTC CTTTCCAACAACCTGAACAAATTTGATGAAGTAT	1281
	ATACTTCATCAAATTTGTTTCAGGTTGTTGGAAAGGAGACTAAC AAGTTGTCCAATACTTATTTTATCTAGAACACGGCTTGACAGC TTTAAAGTCTAAAAGAAAAATGGAAAGTTAGATAA	1282
	TAGATAAAAATAAGTATT	1283
	AATACTTATTTTATCTA	1284
Cystic fibrosis Gly178Arg GGA to AGA	TTTCCATTTTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCT AGATAAAAATAAGTATTGGACAACCTGTTAGTCTCCTTTCCAAC AACCTGAACAAATTTGATGAAGTATGTACCTATT	1285
	AATAGGTACATACTTCATCAAATTTGTTTCAGGTTGTTGGAAAG GAGACTAACAAGTTGTCCAATACTTATTTTATCTAGAACACGG CTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA	1286
	TAAGTATTGGACAACCT	1287
	AAGTTGTCCAATACTTA	1288
Cystic fibrosis His199Gln CAT to CAG	AAGATACAATGACACCTGTTTTTGCTGTGCTTTTATTTTCCAG GGACTTGCAATTGGCACATTCGTGTGGATCGCTCCTTTGCAA GTGGCACTCCTCATGGGGCTAATCTGGGAGTTGTTA	1289

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAA AGGAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGA AAATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTT	1290
	TTGGCACATTTCGTGTG	1291
	CACACGAAATGTGCCAA	1292
Cystic fibrosis His199Tyr CAT to TAT	GGAAGATAACAATGACACCTGTTTTGCTGTGCTTTTATTTTCC AGGGACTTGCAATTGGCAGATTTCGTGTGGATCGCTCCTTTGC AAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTGT	1293
	ACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAG GAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGAAA ATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTTCC	1294
	CATTGGCAGATTTCGTG	1295
	CACGAAATGTGCCAATG	1296
Cystic fibrosis Pro205Ser CCT to TCT	TGTTTTGCTGTGCTTTTATTTTCCAGGGACTTGCAATTGGCAC ATTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGG GGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCT	1297
	AGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCATG AGGAGTGCCACTTGCAAAGGAGCGATCCACACGAAATGTGC CAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAAAACA	1298
	GGATCGCTCCTTTGCAA	1299
	TTGCAAAGGAGCGATCC	1300
Cystic fibrosis Leu206Trp TTG to TGG	TTTGCTGTGCTTTTATTTTCCAGGGACTTGCAATTGGCACATT CGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGGGC TAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGG	1301
	CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAGGAGCGATCCACACGAAAT GTGCCAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAA	1302
	CGCTCCTTTGCAAGTGG	1303
	CCACTTGCAAAGGAGCG	1304
Cystic fibrosis Gln220Term CAG to TAG	TTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGG GCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGGACT TGGTTTCCTGATAGTCCTTGCCCTTTTTCAGGCTGGGC	1305
	GCCCAGCCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGT CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAGGAGCGATCCACACGAA	1306

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGTTGTTACAGGCGTCT	1307
	AGACGCCTGTAACAACT	1308
Cystic fibrosis Cys225Arg TGT-CGT	CCTTTGCAAGTGGCACTCCTCATGGGGCTAATCTGGGAGTT GTTACAGGCGTCTGCCTTCCTGGACTTGGTTTCCTGATAGT CCTTGCCCTTTTTCAGGCTGGGCTAGGGAGAATGATGA	1309
	TCATCATTCTCCCTAGCCCAGCCTGAAAAGGGCAAGGACTA TCAGGAAACCAAGTCCACAGAAGGCAGACGCCTGTAACAAC TCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAGG	1310
	CTGCCTTCCTGGACTT	1311
	AAGTCCACAGAAGGCAG	1312
Cystic fibrosis Val232Asp GTC to GAC	TGGGGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGT GGACTTGGTTTCCTGATAGTCCTTGCCCTTTTTCAGGCTGGG CTAGGGAGAATGATGATGAAGTACAGGAGCAACCTAT	1313
	ATAGGTTGCTACCTGTACTTCATCATCATTCTCCCTAGCCCA GCCTGAAAAGGGCAAGGACTATCAGGAAACCAAGTCCACA GAAGGCAGACGCCTGTAACAACCTCCAGATTAGCCCCA	1314
	CCTGATAGTCCTTGCCC	1315
	GGGCAAGGACTATCAGG	1316
Cystic fibrosis Gly239Arg GGG to AGG	GTTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGT CCTTGCCCTTTTTCAGGCTGGGCTAGGGAGAATGATGATGAA GTACAGGTAGCAACCTATTTTCATAACTTGAAAGTTT	1317
	AACTTTCAAGTTATGAAAATAGGTTGCTACCTGTACTTCATC ATCATTCTCCCTAGCCCAGCCTGAAAAGGGCAAGGACTATC AGGAAACCAAGTCCACAGAAGGCAGACGCCTGTAAC	1318
	TTTCAGGCTGGGCTAGG	1319
	CCTAGCCCAGCCTGAAA	1320

EXAMPLE 10**Cyclin-dependent kinase inhibitor 2A - CDKN2A**

The human CDKN2A gene was also designated MTS-1 for multiple tumor suppressor-1 and has been implicated in multiple cancers including, for example, malignant melanoma. Malignant melanoma is a cutaneous neoplasm of melanocytes. Melanomas generally have features of asymmetry, irregular border, variegated color, and diameter greater than 6 mm. The precise cause of melanoma is

unknown, but sunlight and heredity are risk factors. Melanoma has been increasing during the past few decades.

The CDKN2A gene has been found to be homozygously deleted at high frequency in cell lines derived from tumors of lung, breast, brain, bone, skin, bladder, kidney, ovary, and lymphocyte. Melanoma cell lines carried at least one copy of CDKN2A in combination with a deleted allele. Melanoma cell lines that carried at least 1 copy of CDKN2A frequently showed nonsense, missense, or frameshift mutations in the gene. Thus, CDKN2A may rival p53 (see Example 5) in the universality of its involvement in tumorigenesis. The attached table discloses the correcting oligonucleotide base sequences for the CDKN2A oligonucleotides of the invention.

Table 17
CDKN2A Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Melanoma Trp15Term TGG-TAG	GGGCGGCGGGGAGCAGCATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGG	1321
	CCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCGGCTCCATGCTGCTCCCCGCCGCC	1322
	GGCTGACTGGCTGGCCA	1323
	TGGCCAGCCAGTCAGCC	1324
Melanoma Leu16Pro CTG-CCG	CGGCGGGGAGCAGCATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCTGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGC	1325
	GCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACC CGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCGGCTCCATGCTGCTCCCCGCCG	1326
	TGACTGGCTGGCCACGG	1327
	CCGTGGCCAGCCAGTCA	1328
Melanoma Gly23Asp GGT-GAT	CGGCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCTGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTGCCAACGCACCGAATAG	1329
	CTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGCGCCGCACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCA GCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCGCC	1330
	GGCCCGGGGTCGGGTAG	1331

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTACCCGACCCCGGGCC	1332
Melanoma Arg24Pro CGG-CCG	CGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCC ACGGCCGCGGCCCGGGGT <u>C</u> GGTAGAGGAGGTGCGGGCGC TGCTGGAGGCGGGGGCGCTGCCAACGCACCGAATAGTTA	1333
	TAACTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGC GCCCCGACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGC CAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCG	1334
	CCGGGGT <u>C</u> GGTAGAGG	1335
	CCTCTACCCGACCCCGG	1336
Melanoma Leu32Pro CTG-CCG	CGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCTGGGT AGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTGCCC AACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTGGG	1337
	CCCACCTGGATCGGCCTCCGACCGTAACTATTCGGTGCGTTG GGCAGCGCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTAC CCGACCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCG	1338
	GGCGCTGCTGGAGGCGG	1339
	CCGCCTCCAGCAGCGCC	1340
Melanoma Gly35Ala GGG-GCG	GGCTGGCCACGGCCGCGGCCCGGGGTCTGGGTAGAGGAGGT GCGGGCGCTGCTGGAGGCGGGGGCGCTGCCAACGCACCG AATAGTTACGGTCGGAGGCCGATCCAGGTGGGTAGAGGGTC	1341
	GACCCTCTACCCACCTGGATCGGCCTCCGACCGTAACTATTC GGTGCGTTGGGCAGCGCCCGCCTCCAGCAGCGCCCGCAC CTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCC	1342
	GGAGGCGGGGGCGCTGC	1343
	GCAGCGCCCGCCTCC	1344
Melanoma Tyr44Term TACg-TAA	GGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTG CCCAACGCACCGAATAGTTA <u>C</u> GGTCGGAGGCCGATCCAGGTG GGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGA	1345
	TCGCCCCGCATCCCCGCTCCCGCTGCAGACCCTCTACCCAC CTGGATCGGCCTCCGACCGTAACTATTCGGTGCGTTGGGCAG CGCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACC	1346
	AATAGTTA <u>C</u> GGTCGGAG	1347
	CTCCGACCGTAACTATT	1348
Melanoma Met53Ile ATGa-ATC	TCTCCCATACCTGCCCCCACCCTGGCTCTGACCACTCTGCTC TCTCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGG AGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCA	1349
	TGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCG CCACGCGGGCGCTGCCCATCATCAAGACCTGCCAGAGAGAG CAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGGAGA	1350
	GTCATGATGATGGGCAG	1351

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CTGCCCATCATCATGAC	1352
Melanoma Met54Ile ATGg-ATT	CCCATACCTGCCCCCACCCTGGCTCTGACCACTCTGCTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCAGAC	1353
	GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCGCCACGCGGGCGCTGCCCATCATCATGACCTGCCAGAGA GAGCAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGG	1354
	ATGATGATGGGCAGCGC	1355
	GCGCTGCCCATCATCAT	1356
Melanoma Ser56Ile AGC-ATC	GCCGGCCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGC	1357
	GCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCCGGC	1358
	GATGGGCAGCGCCCGAG	1359
	CTCGGGCGCTGCCCATC	1360
Melanoma Ala57Val GCC-GTC	GGCCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC	1361
	GTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCC	1362
	GGGCAGCGCCCGAGTGG	1363
	CCACTCGGGCGCTGCCC	1364
Melanoma Arg58Term cCGA-TGA	CCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTC	1365
	GAGTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGG	1366
	GCAGCGCCCGAGTGGCG	1367
	CGCCACTCGGGCGCTGC	1368
Melanoma Val59Gly GTG-GGG	CACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCAC	1369
	GTGAGAGTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGAGCAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTG	1370
	CGCCCGAGTGGCGGAGC	1371

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GCTCCGCCACTCGGGCG	1372
Melanoma Leu62Pro CTG-CCG	TCTGACCACTCTGCTCTCTCTGGCAGGTCATGATGATGGGCA GCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGA GCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGT	1373
	ACCGGTCGGGTGAGAGTGGCAGGGTCTGCGCAGTTGGGCTC CGCGCCGTGGAGCAGCAGCAGCTCCGCCACGCGGGCGCTG CCCATCATCATGACCTGCCAGAGAGAGCAGAGTGGTCAGA	1374
	GGCGGAGCTGCTGCTGC	1375
	GCAGCAGCAGCTCCGCC	1376
Melanoma Ala68Val GCG-GTG	TCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAG CTGCTGCTGCTCCACGGCGCGGAGGCCCAACTGCGCAGACCC TGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGA	1377
	TCCCGGGCAGCATCATGCACCGGTCTGGGTGAGAGTGGCAGG GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCCCATCATCATGACCTGCCAGA	1378
	CCACGGCGCGGAGCCCA	1379
	TGGGCTCCGCGCCGTGG	1380
Melanoma Asn71Lys AACT-AAA	CATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGC TCCACGGCGCGGAGGCCCAACTGCGCCGACCCCGCCACTCTC ACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTG	1381
	CAGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCTGGGTGA GAGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATG	1382
	GAGCCCAACTGCGCCGA	1383
	TCGGCGCAGTTGGGCTC	1384
Melanoma Asn71Ser AAC-AGC	TCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGGCCCAACTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCT	1385
	AGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCTGGGTGAG AGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGA	1386
	GGAGCCCAACTGCGCCG	1387
	CGGCGCAGTTGGGCTCC	1388
Melanoma Pro81Leu CCC-CTC	AGCTGCTGCTGCTCCACGGCGCGGAGGCCCAACTGCGCCGAC CCCGCCACTCTCACCCGACCGTGCACGACGCTGCCCGGGA GGGCTTCCTGGACACGCTGGTGGTGTGCACCGGGCCGG	1389
	CCGGCCCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTC CCGGGCAGCGTCGTGCACGGGTCTGGGTGAGAGTGGCGGGG TCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT	1390
	CACCCGACCGTGCACG	1391

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGTGCACGGGTCGGGTG	1392
Melanoma Asp84Tyr cGAC-TAC	CTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC TCTACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCC TGGACACGCTGGTGGTGTGTCACCGGGCCGGGGCGCGGC	1393
	GCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCCAGG AAGCCCTCCCGGGCAGCGTGTGTCACGGGTGCGGTGAGAGT GGCGGGGTGCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAG	1394
	CCGTGCACGACGCTGCC	1395
	GGCAGCGTGTGTCACGG	1396
Melanoma Ala85Thr cGCT-ACT	CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGG ACACGCTGGTGGTGTGTCACCGGGCCGGGGCGCGGCTGG	1397
	CCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCC AGGAAGCCCTCCCGGGCAGCGTGTGTCACGGGTGCGGTGAG AGTGGCGGGGTGCGGCGCAGTTGGGCTCCGCGCCGTGGAG	1398
	TGCACGACGCTGCCCGG	1399
	CCGGGCAGCGTGTGCA	1400
Melanoma Arg87Pro CGG-CCG	GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGA CCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGGACACGCT GGTGGTGTGTCACCGGGCCGGGGCGCGGCTGGACGTGCG	1401
	CGCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCCCGGGCAGCGTGTGTCACGGGTG GGGTGAGAGTGGCGGGGTGCGGCGCAGTTGGGCTCCGCGC	1402
	CGCTGCCCGGGAGGGCT	1403
	AGCCCTCCCGGGCAGCG	1404
Melanoma Arg87Trp cCGG-TGG	GGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCG ACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGGACACGC TGGTGGTGTGTCACCGGGCCGGGGCGCGGCTGGACGTGC	1405
	GCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGC GTGTCCAGGAAGCCCTCCCGGGCAGCGTGTGTCACGGGTG GGTGAGAGTGGCGGGGTGCGGCGCAGTTGGGCTCCGCGCC	1406
	ACGCTGCCCGGGAGGGC	1407
	GCCCTCCCGGGCAGCGT	1408
Melanoma Leu97Arg CTG-CGG	CTCTACCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTC CTGGACACGCTGGTGGTGTGTCACCGGGCCGGGGCGCGGCT GGACGTGCGCGATGCCTGGGGTGTGCTGCCCGTGGACTT	1409
	AAGTCCACGGGCAGACGACCCAGGCATCGCGCACGTCCAG CCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCCAGGA AGCCCTCCCGGGCAGCATCATGCACCGGTGCGGTGAGAG	1410
	GGTGGTGTGTCACCGGG	1411

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCCGGTGCAGCACCACC	1412
Melanoma Arg99Pro CGG-CCG	CCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGAC ACGCTGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGGACG TGCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGA	1413
	TCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCGCGCAC GTCCAGCCGCGCCCCGGCCGGTGCAGCACCACCAGCGTGT CCAGGAAGCCCTCCCGGGCAGCATCATGCACCGGTCTGGG	1414
	GCTGCACCGGGCCGGGG	1415
	CCCCGGCCCGGTGCAGC	1416
Melanoma Gly101Trp cGGG-TGG	CCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGACACGCT GGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGGACGTGCGC GATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGC	1417
	GCTCCTCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCG CGCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCCCGGGCAGCATCATGCACCGG	1418
	ACCGGGCCGGGGCGCGG	1419
	CCGCGCCCCGGCCCGGT	1420
Melanoma Arg107Cys gCGC-TGC	CGGGAGGGCTTCCTGGACACGCTGGTGGTGTCTGCACCGGGC CGGGGCGCGGCTGGACGTGCGCGATGCCTGGGGTCGTCTGC CCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTG	1421
	CAACGTCGCGGTGGCCCCGCTCCTCGGCCAAGTCCACGGGC AGACGACCCCAGGCATCGCGCACGTCCAGCCGCGCCCCGGC CCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTCCCG	1422
	TGGACGTGCGCGATGCC	1423
	GGCATCGCGCACGTCCA	1424
Melanoma Ala118Thr gGCT-ACT	CACCGGGCCGGGGCGCGGCTGGACGTGCGCGATGCCTGGG GCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGC GATGTCGCACGGTACCTGCGCGCGGCTGCGGGGGGCACCA	1425
	TGGTGCCCCCGCAGCCGCGCGCAGGTACCGTGCGACATCG CGATGGCCCAGCTCCTCAGCCAGGTCCACGGGCAGACGGCC CCAGGCATCGCGCACGTCCAGCCGCGCCCCGGCCCGGTG	1426
	TGGACCTGGCTGAGGAG	1427
	CTCCTCAGCCAGGTCCA	1428
Melanoma Val126Asp GTC-GAC	TGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAG GAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGC TGCGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGA	1429
	TCTATGCGGGCATGGTTACTGCCTCTGGTGCCCCCGCAGCC GCGCGCAGGTACCGTGCGACATCGCGATGGCCCAGCTCCTC AGCCAGGTCCACGGGCAGACGGCCCCAGGCATCGCGCA	1430
	TCGCGATGTCGCACGGT	1431

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACCGTGCGACATCGCGA	1432

EXAMPLE 11**Adenomatous polyposis of the colon - APC**

Adenomatous polyposis of the colon is characterized by adenomatous polyps of the colon and rectum; in extreme cases the bowel is carpeted with a myriad of polyps. This is a viciously premalignant disease with one or more polyps progressing through dysplasia to malignancy in untreated gene carriers with a median age at diagnosis of 40 years.

Mutations in the APC gene are an initiating event for both familial and sporadic colorectal tumorigenesis and many alleles of the APC gene have been identified. Carcinoma may arise at any age from late childhood through the seventh decade with presenting features including, for example, weight loss and inanition, bowel obstruction, or bloody diarrhea. Cases of new mutation still present in these ways but in areas with well organized registers most other gene carriers are detected. The attached table discloses the correcting oligonucleotide base sequences for the APC oligonucleotides of the invention.

Table 18
APC Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Adenomatous polyposis coli Arg121Term AGA-TGA	GGATCTGTATCAAGCCGTTCTGGAGAGTGCAAGTCCTGTTCTT ATGGGTTTCATTTCCAAGAAGAGGGTTTGTAAATGGAAGCAGA GAAAGTACTGGATATTTAGAAGAACTTGAGAAAGAGA	1433
	TCTCTTTCTCAAGTTCTTCTAAATATCCAGTACTTTCTCTGCTT CCATTTACAAACCCTCTTCTTGAAATGAACCCATAGGAACAG GACTGCACTCTCCAGAACGGCTTGATACAGATCC	1434
	TTCCAAGAAGAGGGTTT	1435
	AAACCCTCTTCTTGGA	1436
Adenomatous polyposis coli Trp157Term TGG-TAG	AAAAAAAAAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAA GAAAAGGAAAAAGACTGGTATTACGCTCAACTTCAGAATCTCA CTAAAAGAATAGATAGTCTTCCTTTAACTGAAAA	1437
	TTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTG AAGTTGAGCGTAATACCAGTCTTTTCTTTCTTTCTTTGTCAA GATCAGCAAGAAGCAATGACCTATTTTTTTTTT	1438
	AAAAGACTGGTATTACG	1439
	CGTAATACCAGTCTTTT	1440
Adenomatous polyposis coli Tyr159Term TAC-TAG	AAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAAGAAAAG GAAAAGACTGGTATTACGCTCAACTTCAGAATCTCACTAAAA GAATAGATAGTCTTCCTTTAACTGAAAATGTAAGT	1441
	ACTTACATTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGA GATTCTGAAGTTGAGCGTAATACCAGTCTTTTCTTTCTTTCTTCT TTGTCAAGATCAGCAAGAAGCAATGACCTATTT	1442
	TGGTATTACGCTCAACT	1443
	AGTTGAGCGTAATACCA	1444
Adenomatous polyposis coli Gln163Term CAG-TAG	TTGCTTCTTGCTGATCTTGACAAAGAAGAAAAGGAAAAAGACT GGTATTACGCTCAACTTCAGAATCTCACTAAAAGAATAGATAG TCTTCCTTTAACTGAAAATGTAAGTAACTGGCAGT	1445
	ACTGCCAGTTACTTACATTTTCAGTTAAAGGAAGACTATCTATT CTTTTAGTGAGATTCTGAAGTTGAGCGTAATACCAGTCTTTTTC CTTTCTTCTTTGTCAAGATCAGCAAGAAGCAA	1446
	CTCAACTTCAGAATCTC	1447
	GAGATTCTGAAGTTGAG	1448
Adenomatous polyposis coli Arg168Term AGA-TGA	CTTGACAAAGAAGAAAAGGAAAAAGACTGGTATTACGCTCAAC TTCAGAATCTCACTAAAAGAATAGATAGTCTTCCTTTAACTGAA AATGTAAGTAACTGGCAGTACAACCTATTTGAAA	1449
	TTTCAAATAAGTTGTACTGCCAGTTACTTACATTTTCAGTTAAA GGAAGACTATCTATTCTTTTAGTGAGATTCTGAAGTTGAGCGT AATACCAGTCTTTTCTTTCTTTCTTTGTCAAG	1450

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TCACTAAA <u>A</u> GAATAGAT	1451
	ATCTATTCTTTTAGTGA	1452
Adenomatous polyposis coli Ser171Ile AGT-ATT	AAGAAAAGGAAAAAGACTGGTATTACGCTCAACTTCAGAATCT CACTAAAAGAATAGATAGTCTTCCTTTAACTGAAAATGTAAGTA ACTGGCAGTACAACCTTATTTGAACTTTAATAAC	1453
	GTTATTAAAGTTTCAAATAAGTTGACTGCCAGTTACTTACATT TTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTGAA GTTGAGCGTAATACCAGTCTTTTTCCTTTTCTT	1454
	AATAGATAGTCTTCCTT	1455
	AAGGAAGACTATCTATT	1456
Adenomatous polyposis coli Gln181Term CAA-TAA	GATTAACGTAAATACAAGATATTGATACTTTTTATTATTTGTGG TTTTAGTTTTCTTACAACAGATATGACCAGAAGGCAATTGG AATATGAAGCAAGGCAAATCAGAGTTGCGATGG	1457
	CCATCGCAACTCTGATTTGCCTTGCTTCATATTCCAATTGCCT TCTGGTCATATCTGTTTGTAAAGGAAAACATAACCACAAATAAT AAAAAAGTATCAATATCTTGTATTTACGTTAATC	1458
	TTTCCTTACAACAGAT	1459
	ATCTGTTTGTAAAGGAAA	1460
Adenomatous polyposis coli Glu190Term GAA-TAA	CTTTTTATTATTTGTGGTTTTAGTTTTCTTACAACAGATATG ACCAGAAGGCAATTGGAATATGAAGCAAGGCAAATCAGAGTT GCGATGGAAGAACAACCTAGGTACCTGCCAGGATA	1461
	TATCCTGGCAGGTACCTAGTTGTTCTTCCATCGCAACTCTGAT TTGCCTTGCTTCATATTCCAATTGCCTTCTGGTCATATCTGTTT GTAAGGAAAACATAACCACAAATAATAAAAAAG	1462
	GGCAATTGGAATATGAA	1463
	TTCATATTCCAATTGCC	1464
Adenomatous polyposis coli Gln208Term CAG-TAG	CAATTGGAATATGAAGCAAGGCAAATCAGAGTTGCGATGGAA GAACAACCTAGGTACCTGCCAGGATATGGAAAAACGAGCACAG GTAAGTTACTTGTTTCTAAGTGATAAAACAGCGAAGA	1465
	TCTTCGCTGTTTTATCACTTAGAAACAAGTAACTTACCTGTGCT CGTTTTTCCATATCCTGGCAGGTACCTAGTTGTTCTTCCATCG CAACTCTGATTTGCCTTGCTTCATATTCCAATTG	1466
	GTACCTGCCAGGATATG	1467
	CATATCCTGGCAGGTAC	1468
Adenomatous polyposis coli Arg213Term CGA-TGA	GCAAGGCAAATCAGAGTTGCGATGGAAGAACAACCTAGGTACC TGCCAGGATATGGAAAAACGAGCACAGGTAAGTTACTTGTTTC TAAGTGATAAAACAGCGAAGAGCTATTAGGAATAAA	1469
	TTTATTCCTAATAGCTCTTCGCTGTTTTATCACTTAGAAACAAG TAACTTACCTGTGCTCGTTTTTCCATATCCTGGCAGGTACCTA GTTGTTCTTCCATCGCAACTCTGATTTGCCTTGC	1470
	TGGAAAAACGAGCACAG	1471
	CTGTGCTCGTTTTTCCA	1472

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Arg232Term CGA-TGA	GTTTTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAA AGGACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAAC AGAAGCAGAGGTTAGTAAATTGCCTTTCTTGTTTG	1473
	CACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGCTTG CCTGTAAAAGCTGTCGTATACGAAGTATGTCCTTTTCGATT TGCTGAATTCTGGCTATTCTTCGCTAAAATAAAC	1474
	TTCGTATACGACAGCTT	1475
	AAGCTGTCGTATACGAA	1476
Adenomatous polyposis coli Gln233Term CAG-TAG	TTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAAAGG ACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAACAGA AGCAGAGGTTAGTAAATTGCCTTTCTTGTTTGTTGG	1477
	CCACAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGC TTGGGACTGTAAAAGCTGTCGTATACGAAGTATGTCCTTTTCG ATTTGCTGAATTCTGGCTATTCTTCGCTAAAATAA	1478
	GTATACGACAGCTTTTA	1479
	TAAAAGCTGTCGTATAC	1480
Adenomatous polyposis coli Gln247Term CAG-TAG	AGAAAGCCTACACCATTTTTGCATGTACTGATGTTAACTCCAT CTTAACAGAGGTCATCTCAGAACAAGCATGAAACCGGCTCAC ATGATGCTGAGCGGCAGAATGAAGGTCAAGGAGTGG	1481
	CCACTCCTTGACCTTCATTCTGCCGCTCAGCATCATCTGAGC CGGTTTCATGCTTGTTCTGAGATGACCTCTGTTAACGGAGT TAACATCAGTACATGCAAAAATGGTGTAGGCTTTCT	1482
	GGTCATCTCAGAACAAG	1483
	CTTGTTCTGAGATGACC	1484
Adenomatous polyposis coli Gly267Term GGA-TGA	CAGAACAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAG AATGAAGGTCAAGGAGTGGGAGAAATCAACATGGCAACTTCT GGTAATGGTCAGGTAAATAAATTATTTATCATATTT	1485
	AAATATGATAAAATAATTTATTTACCTGACCATTACCAGAAGTT GCCATGTTGATTTCTCCCACTCCTTGACCTTCATTCTGCCGCT CAGCATCATGTGAGCCGGTTTCATGCTTGTTCTG	1486
	AAGGAGTGGGAGAAATC	1487
	GATTTCTCCCACTCCTT	1488
Adenomatous polyposis coli Glu443Term GAA-TAA	CTTCAAATAACAAAGCATTATGGTTTATGTTGATTTTATTTTCA GTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGTGT GTTCTAATGAACTTTCAATTTGATGAAGAGCATA	1489
	TATGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCA GGACAGATCTGATGTTCAACAGGAGCTGGCACTGAAAAATAA AATCAACATAAACCATAATGCTTTGTTATTTGAAG	1490
	CTCCTGTTGAACATCAG	1491
	CTGATGTTCAACAGGAG	1492
Adenomatous polyposis coli SER457TER TCA-TAA	CAGTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGT GTGTTCTAATGAACTTTCAATTTGATGAAGAGCATAGACATGC AATGAATGAACTAGGTAAGACAAAAATGTTTTTAA	1493

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTAAAAACATTTTGTCTTACCTAGTTCATTTCATTGCATGTCTA TGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCAG GACAGATCTGATGTTCAACAGGAGCTGGCACTG	1494
	GAACTTTTCATTGATG	1495
	CATCAAATGAAAGTTTC	1496
Adenomatous polyposis coli Gln473Term CAG-TAG	AGTTGTTTTATTTTAGATGATTGTCTTTTCCTCTTGCCCTTTT AAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAAGTG GACTGTGAAATGTACGGGCTTACTAATGACCACT	1497
	AGTGGTCATTAGTAAGCCCGTACATTTACAGTCCACTTGCAA TAATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAAAGGGCA AGAGGAAAAAGACAATCATCTAAATAAAACAAC	1498
	GGGGACTACAGGCCATT	1499
	AATGGCCTGTAGTCCCC	1500
Adenomatous polyposis coli Tyr486Term TAC-TAG	TTTTAAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAA GTGGACTGTGAAATGTACGGGCTTACTAATGACCACTACAGTA TTACACTAAGACGATATGCTGGAATGGCTTTGACA	1501
	TGTCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAG TGGTCATTAGTAAGCCCGTACATTTACAGTCCACTTGCAATA ATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAA	1502
	GAAATGTACGGGCTTAC	1503
	GTAAGCCCGTACATTC	1504
Adenomatous polyposis coli Arg499Term CGA-TGA	TTGCAAGTGGACTGTGAAATGTATGGGCTTACTAATGACCACT ACAGTATTACACTAAGACGATATGCTGGAATGGCTTTGACAAA CTTGACTTTTGGAGATGTAGCCAACAAGGTATGTT	1505
	AACATACCTTGTTGGCTACATCTCCAAAAGTCAAGTTTGTCAA AGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGTGGTCA TTAGTAAGCCCATACATTTACAGTCCACTTGCAA	1506
	CACTAAGACGATATGCT	1507
	AGCATATCGTCTTAGTG	1508
Adenomatous polyposis coli Tyr500Term TAT-TAG	AGTGGACTGTGAAATGTATGGGCTTACTAATGACCACTACAGT ATTACACTAAGACGATATGCTGGAATGGCTTTGACAACTTGA CTTTTGGAGATGTAGCCAACAAGGTATGTTTTAT	1509
	ATAAAAACATACCTTGTTGGCTACATCTCCAAAAGTCAAGTTTG TCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGTG GTCATTAGTAAGCCCATACATTTACAGTCCACT	1510
	AGACGATATGCTGGAAT	1511
	ATTCCAGCATATCGTCT	1512
Adenomatous polyposis coli Lys586Term AAA-TAA	GACAAATCCAACCTCTAATTAGATGACCCATATTCTGTTTCTTA CTAGGAATCAACCCTCAAAGCGTATTGAGTGCCTTATGGAAT TTGTCAGCACATTGCACTGAGAATAAAGCTGATA	1513
	TATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAA GGCACTCAATACGCTTTTGAGGGTTGATTCTAGTAAGAAACA GAATATGGGTCATCTAATTAGAGTTGGAATTTGTC	1514
	CAACCCTCAAAGCGTA	1515

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TACGCTTTTGAGGGTTG	1516
Adenomatous polyposis coli Leu592Term TTA-TGA	TAGATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAA AGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTG AGAATAAAGCTGATATATGTGCTGTAGATGGTGC	1517
	GCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGCAAT GTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAGGGT TGATTCCTAGTAAGAAACAGAATATGGGTCATCTA	1518
	GAGTGCCTTATGGAATT	1519
	AATTCATAAGGCACTC	1520
Adenomatous polyposis coli Trp593Term TGG-TAG	ATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAAG CGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAG AATAAAGCTGATATATGTGCTGTAGATGGTGCCT	1521
	AGTGCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGC AATGTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAG GGTTGATTCCTAGTAAGAAACAGAATATGGGTCAT	1522
	TGCCTTATGGAATTTGT	1523
	ACAAATTCCATAAGGCA	1524
Adenomatous polyposis coli Trp593Term TGG-TGA	TGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAAGC GTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGA ATAAAGCTGATATATGTGCTGTAGATGGTGCCTT	1525
	AAGTGCACCATCTACAGCACATATATCAGCTTTATTCTCAGTG CAATGTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGA GGGTTGATTCCTAGTAAGAAACAGAATATGGGTCA	1526
	GCCTTATGGAATTTGTC	1527
	GACAAATTCCATAAGGC	1528
Adenomatous polyposis coli Tyr622Term TAC-TAA	TAAAGCTGATATATGTGCTGTAGATGGTGCCTTGCATTTTGG GTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCC ATTATTGAAAGTGAGGTTGGGATATTACGGAATGTG	1529
	CACATTCCGTAATATCCACCTCCACTTTCAATAATGGCTAAA GTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAACCAAAAAT GCAAGTGCACCATCTACAGCACATATATCAGCTTTA	1530
	CTTACTTACCGGAGCCA	1531
	TGGCTCCGGTAAGTAAG	1532
Adenomatous polyposis coli Gln625Term CAG-TAG	GATATATGTGCTGTAGATGGTGCCTTGCATTTTGGTTGGCA CTCTTACTTACCGGAGCCAGACAAACACTTTAGCCATTATTGA AAGTGGAGGTGGGATATTACGGAATGTGTCCAGCT	1533
	AGCTGGACACATTCCGTAATATCCACCTCCACTTTCAATAAT GGCTAAAGTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAAC CAAAAATGCAAGTGCACCATCTACAGCACATATATC	1534
	ACCGGAGCCAGACAAAC	1535
	GTTTGTCTGGCTCCGGT	1536

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Adenomatous polyposis coli Leu629Term TTA-TAA	TAGATGGTGCACCTTGCATTTTTGGTTGGCACTCTTACTTACCG GAGCCAGACAAACACTTTAGCCATTATTGAAAGTGGAGGTGG GATATTACGGAATGTGTCCAGCTTGATAGCTACAAA	1537
	TTGTAGCTATCAAGCTGGACACATTCCGTAATATCCCACCTC CACTTTCAATAATGGCTAAAGTGTTTGTCTGGCTCCGGTAAGT AAGAGTGCCAACCAAAAATGCAAGTGCACCATCTA AAACACTTTAGCCATTA TAATGGCTAAAGTGTTT	1538 1539 1540
Adenomatous polyposis coli Glu650Term GAG-TAG	GCCATTATTGAAAGTGGAGGTGGGATATTACGGAATGTGTCC AGCTTGATAGCTACAAATGAGGACCACAGGTATATATAGAGTT TTATATTACTTTTAAAGTACAGAATTCATACTCTCA TGAGAGTATGAATTCTGTACTTTAAAAGTAATATAAACTCTAT ATATACCTGTGGTCCTCATTGTAGCTATCAAGCTGGACACAT TCCGTAATATCCCACCTCCACTTTCAATAATGGC CTACAAATGAGGACCAC GTGGTCCTCATTGTAG	1541 1542 1543 1544
	TGCATGTGGAACCTTGTGGAATCTCTCAGCAAGAAATCCTAAA GACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGCTC AAGAACCTCATTCAATCAAAGCACAAAATGATTGCT AGCAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATG CTAACTGCCCCCATGTCCATAATGCTTCCTGGTCTTTAGGAT TTCTTGCTGAGAGATTCCACAAAGTTCCACATGCA GCATTATGGGACATGGG CCCATGTCCATAATGC	1545 1546 1547 1548
	AAGACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGC TCAAGAACCTCATTCAATCAAAGCACAAAATGATTGCTATGGG AAGTGCTGCAGCTTTAAGGAATCTCATGGCAAATAG CTATTTGCCATGAGATTCCTTAAAGCTGCAGCACTTCCCATAG CAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATGCT AACTGCCCCCATGTCCATAATGCTTCCTGGTCTT CATTCAATCAAAGCACA TGTGCTTTGAATGAATG	1549 1550 1551 1552
	GGGGCAGTTAGCATGCTCAAGAACCTCATTCAATCAAAGCAC AAAATGATTGCTATGGGAAGTGCTGCAGCTTTAAGGAATCTCA TGGCAAATAGGCCTGCGAAGTACAAGGATGCCAATA TATTGGCATCCTTGTACTTCGCAGGCCTATTTGCCATGAGATT CCTTAAAGCTGCAGCACTTCCCATAGCAATCATTTTGTGCTTT GAATGAATGAGGTTCTTGAGCATGCTAACTGCCCC CTATGGGAAGTGCTGCA TGCAGCACTTCCCATAG	1553 1554 1555 1556

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Adenomatous polyposis coli Leu764Term TTA-TAA	TCTCCTGGCTCAGCTTGCCATCTCTTCATGTTAGGAAACAAA AGCCCTAGAAGCAGAATTAGATGCTCAGCACTTATCAGAACT TTTGACAATATAGACAATTTAAGTCCCAAGGCATC	1557
	GATGCCTTGGGACTTAAATTGTCTATATTGTCAAAGTTTCTGA TAAGTGCTGAGCATCTAATTCTGCTTCTAGGGCTTTTTGTTTC CTAACATGAAGAGATGGCAAGCTGAGCCAGGAGA	1558
	AGCAGAATTAGATGCTC	1559
	GAGCATCTAATTCTGCT	1560
Adenomatous polyposis coli Ser784Thr TCT-ACT	TTAGATGCTCAGCACTTATCAGAACTTTTGACAATATAGACAA TTTAAGTCCCAAGGCATCTCATCGTAGTAAGCAGAGACACAG CAAGTCTCTATGGTGATTATGTTTTTGACACCATC	1561
	GATGGTGTCAAAAACATAATCACCATAGAGACTTGCTGTGTCT CTGCTTACTACGATGAGATGCCTTGGGACTTAAATTGTCTATA TTGTCAAAGTTTCTGATAAGTGCTGAGCATCTAA	1562
	CCAAGGCATCTCATCGT	1563
	ACGATGAGATGCCTTGG	1564
Adenomatous polyposis coli Arg805Term CGA-TGA	CTCATCGTAGTAAGCAGAGACACAGCAAGTCTCTATGGTGATT ATGTTTTTGACACCAATCGACATGATGATAATAGGTCAGACAT TTTAATACTGGCACATGACTGTCCTTTCACCATAT	1565
	ATATGGTGAAAGGACAGTCATGTGCCAGTATTAAATGTCTG- CCTATTATCATCATGTGCGATTGGTGTCAAAAACATAATCACCAT AGAGACTTGCTGTGTCTCTGCTTACTACGATGAG	1566
	ACACCAATCGACATGAT	1567
	ATCATGTGCGATTGGTGT	1568
Adenomatous polyposis coli Gln879Term CAG-TAG	GGTCTAGGCAACTACCATCCAGCAACAGAAAATCCAGGAACT TCTTCAAAGCGAGGTTTGCGAGATCTCCACCACTGCAGCCCAG ATTGCCAAAGTCATGGAAGAAGTGTCAGCCATTCTATA	1569
	TATGAATGGCTGACACTTCTTCCATGACTTTGGCAATCTGGGC TGCAGTGGTGGAGATCTGCAAACCTCGCTTTGAAGAAGTTCC TGGATTTTCTGTTGCTGGATGGTAGTTGCCTAGACC	1570
	GAGGTTTGCAGATCTCC	1571
	GGAGATCTGCAAACCTC	1572
Adenomatous polyposis coli Ser932Term TCA-TAA	TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTC GAAAATTCAAATAGGACATGTTCTATGCCTTATGC	1573
	GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTTTGAATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA	1574
	TACACATTCAAACACTT	1575
	AAGTGTTTGAATGTGTA	1576
Adenomatous polyposis coli Ser932Term TCA-TGA	TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC	1577

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCATAAGGCATAGAACATGTCCTATTTGAATTTCCGACTTAG TGAAATTGTAAGTGTTGAATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA	1578
	TACACATTCAAACACTT	1579
	AAGTGTTTGAATGTGTA	1580
Adenomatous polyposis coli Tyr935Term TAC-TAG	GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCA TACACATTCAAACACTTACAATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA	1581
	TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTT CCGACTTAGTGAAATTGTAAGTGTTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC	1582
	AACACTTACAATTTTAC	1583
	GTGAAATTGTAAGTGTT	1584
Adenomatous polyposis coli Tyr935Term TAC-TAA	GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCA TACACATTCAAACACTTACAATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA	1585
	TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTT CCGACTTAGTGAAATTGTAAGTGTTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC	1586
	AACACTTACAATTTTAC	1587
	GTGAAATTGTAAGTGTT	1588
Adenomatous polyposis coli Tyr1000Term TAC-TAA	ACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTAAGTTTT GCAGTTATGGTCAATACCCAGCCGACCTAGCCCATAAAATACA TAGTGCAAATCATATGGATGATAATGATGGAGAA	1589
	TTCTCCATCATTATCATCCATATGATTTGCACTATGTATTTTAT GGGCTAGGTCGGCTGGGTATTGACCATAACTGCAAACTTAC TTTCATCATCTTCAGAATAGGATTCAATCGAGGGT	1590
	GGTCAATACCCAGCCGA	1591
	TCGGCTGGGTATTGACC	1592
Adenomatous polyposis coli Glu1020Term GAA-TAA	TACCCAGCCGACCTAGCCCATAAAATACATAGTGCAAATCATA TGGATGATAATGATGGAGAACTAGATACACCAATAAATTATAG TCTTAAATATTCAGATGAGCAGTTGAACTCTGGAA	1593
	TTCCAGAGTTCAACTGCTCATCTGAATATTTAAGACTATAATTT ATTGGTGTATCTAGTTCTCCATCATTATCATCCATATGATTTGC ACTATGTATTTTATGGGCTAGGTCGGCTGGGTA	1594
	ATGATGGAGAACTAGAT	1595
	ATCTAGTTCTCCATCAT	1596
Adenomatous polyposis coli Ser1032Term TCA-TAA	ATGAAACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTA AGTTTTGCAGTTATGGTCAATACCCAGCCGACCTAGCCCATAA AATACATAGTGCAAATCATATGGATGATAATGATG	1597
	CATCATTATCATCCATATGATTTGCACTATGTATTTTATGGGCT AGGTCGGCTGGGTATTGACCATAACTGCAAACTTACTTTTAT CATCTTCAGAATAGGATTCAATCGAGGGTTTCAT	1598

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GTTATGGTCAATACCCA	1599
	TGGGTATTGACCATAAC	1600
Adenomatous polyposis coli Gln1041Term CAA-TAA	TGAAGATGATGAAAGTAAGTTTTGCAGTTATGGTCAATACCCA GCCGACCTAGCCCATAAAATACATAGTGCAAATCATATGGATG ATAATGATGGAGAACTAGATACACCAATAAATTAT	1601
	ATAATTTATTGGTGTATCTAGTTCTCCATCATTATCATCCATAT GATTTGCACTATGTATTTTATGGGCTAGGTCTGGCTGGGTATTG ACCATAACTGCAAACTTACTTTTCATCATCTTCA	1602
	GCCCATAAAATACATAG	1603
	CTATGTATTTTATGGGC	1604
Adenomatous polyposis coli Gln1045Term CAG-TAG	ATAAATTATAGTCTTAAATATTCAGATGAGCAGTTGAACTCTGG AAGGCAAAGTCCTTCACAGAATGAAAGATGGGCAAGACCCAA ACACATAATAGAAGATGAAATAAAACAAAGTGAGC	1605
	GCTCACTTTGTTTTATTTTCATCTTCTATTATGTGTTTGGGTCTT GCCCATCTTTCATTCTGTGAAGGACTTTGCCTTCCAGAGTTCA ACTGCTCATCTGAATATTTAAGACTATAATTTAT	1606
	GTCCTTCACAGAATGAA	1607
	TTCATTCTGTGAAGGAC	1608
Adenomatous polyposis coli Gln1067Term CAA-TAA	GAAAGATGGGCAAGACCCAAACACATAATAGAAGATGAAATAA AACAAAGTGAGCAAAGAGAATCAAGGAATCAAAGTACAACCTTA TCCTGTTTATACTGAGAGCACTGATGATAAACACC	1609
	GGTGTTTATCATCAGTGCTCTCAGTATAAACAGGATAAGTTGT ACTTTGATTCCTTGATTGTCTTTGCTCACTTTGTTTTATTTTCATC TTCTATTATGTGTTTGGGTCTTGCCCATCTTTC	1610
	AGCAAAGACAATCAAGG	1611
	CCTTGATTGTCTTTGCT	1612
Adenomatous polyposis coli Tyr1075Term TAT-TAG	AATAGAAGATGAAATAAAACAAAGTGAGCAAAGACAATCAAGG AATCAAAGTACAACCTTATCCTGTTTATACTGAGAGCACTGATG ATAAACACCTCAAGTTCCAACCACATTTTGGACAG	1613
	CTGTCCAAAATGTGGTTGGAAGTTGAGGTGTTTATCATCAGTG CTCTCAGTATAAACAGGATAAGTTGTACTTTGATTCCTTGATTG TCTTTGCTCACTTTGTTTTATTTTCATCTTCTATT	1614
	ACAACCTATCCTGTTTA	1615
	TAAACAGGATAAGTTGT	1616
Adenomatous polyposis coli Tyr1102Term TAC-TAG	TGATGATAAACACCTCAAGTTCCAACCACATTTTGGACAGCAG GAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTTCA GAAACAAATCGAGTGGGTTCTAATCATGGAATTAAT	1617
	ATTAATTCCATGATTAGAACCCACTCGATTTGTTTCTGAACCAT TGGCTCCCCGTGACCTGTATGGAGAAACACATTCCTGCTGTC CAAATGTGGTTGGAAGTTGAGGTGTTTATCATCA	1618
	TCTCCATACAGGTCACG	1619
	CGTGACCTGTATGGAGA	1620

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Ser1110Term TCA-TGA	AACCACATTTTGGACAGCAGGAATGTGTTTCTCCATACAGGTC ACGGGGAGCCAATGGTTGAGAAACAAATCGAGTGGGTTCTAA TCATGGAATTAATCAAAATGTAAGCCAGTCTTTGTG	1621
	CACAAAGACTGGCTTACATTTTGATTAATTCCATGATTAGAACC CACTCGATTTGTTTCTGAACCATTGGCTCCCCGTGACCTGTAT GGAGAAACACATTCTGCTGTCCAAATGTGGTT	1622
	CAATGGTTGAGAAACAA	1623
	TTGTTTCTGAACCATTG	1624
Adenomatous polyposis coli Arg1114Term CGA-TGA	GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCC AATGGTTCAGAAACAAATCGAGTGGGTTCTAATCATGGAATTA ATCAAAATGTAAGCCAGTCTTTGTGTCAAGAAGATG	1625
	CATCTTCTTGACACAAAGACTGGCTTACATTTTGATTAATTCCA TGATTAGAACCCACTCGATTTGTTTCTGAACCATTGGCTCCCC GTGACCTGTATGGAGAAACACATTCTGCTGTCC	1626
	AAACAAATCGAGTGGGT	1627
	ACCCACTCGATTTGTTT	1628
Adenomatous polyposis coli Tyr1135Term TAT-TAG	GGGTTCTAATCATGGAATTAATCAAAATGTAAGCCAGTCTTTG TGTCAGAAGATGACTATGAAGATGATAAGCCTACCAATTATA GTGAACGTTACTCTGAAGAAGAACAGCATGAAGAA	1629
	TTCTTCATGCTGTTCTTCTTCAGAGTAACGTTCACTATAATTGG TAGGCTTATCATCTTCATAGTCATCTTCTTGACACAAAGACTG GCTTACATTTTGATTAATTCCATGATTAGAACCC	1630
	GATGACTATGAAGATGA	1631
	TCATCTTCATAGTCATC	1632
Adenomatous polyposis coli Gln1152Term CAG-TAG	GAAGATGACTATGAAGATGATAAGCCTACCAATTATAGTGAAC GTTACTCTGAAGAAGAACAGCATGAAGAAGAAGAGAGACCAA CAAATTATAGCATAAAATATAATGAAGAGAAACGTC	1633
	GACGTTTCTCTTCATTATATTTATGCTATAATTTGTTGGTCTCT CTTCTTCTTCATGCTGTTCTTCTTCAGAGTAACGTTCACTATAA TTGGTAGGCTTATCATCTTCATAGTCATCTTC	1634
	AAGAAGAACAGCATGAA	1635
	TTCATGCTGTTCTTCTT	1636
Adenomatous polyposis coli Gln1175Term CAG-TAG	GAAGAAGAGAGACCAACAAATTATAGCATAAAATATAATGAAG AGAAACGTCATGTGGATCAGCCTATTGATTATAGTTTAAATAT GCCACAGATATTCCTTCATCACAGAAACAGTCAT	1637
	ATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAAA CTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCATTATA TTTTATGCTATAATTTGTTGGTCTCTCTTCTTC	1638
	ATGTGGATCAGCCTATT	1639
	AATAGGCTGATCCACAT	1640

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Pro1176Leu CCT-CTT	AAGAGAGACCAACAAATTATAGCATAAAATATAATGAAGAGAA ACGTCATGTGGATCAGCCTATTGATTATAGTTTAAATATGCCA CAGATATTCCTTCATCACAGAAACAGTCATTTTC	1641
	GAAAATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATT TTAAACTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCA TTATATTTTATGCTATAATTTGTTGGTCTCTCTT	1642
	GGATCAGCCTATTGATT	1643
	AATCAATAGGCTGATCC	1644
Adenomatous polyposis coli Ala1184Pro GCC-CCC	ATAAAATATAATGAAGAGAAACGTCATGTGGATCAGCCTATTG ATTATAGTTTAAATATGCCACAGATATTCCTTCATCACAGAAA CAGTCATTTTCATTCTCAAAGAGTTCATCTGGAC	1645
	GTCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGA TGAAGGAATATCTGTGGCATATTTTAAACTATAATCAATAGGCT GATCCACATGACGTTTCTCTTCATTATATTTTAT	1646
	TAAAATATGCCACAGAT	1647
	ATCTGTGGCATATTTTA	1648
Adenomatous polyposis coli Ser1194Term TCA-TGA	ATCAGCCTATTGATTATAGTTTAAATATGCCACAGATATTCCT TCATCACAGAAACAGTCATTTTCATTCTCAAAGAGTTCATCTG GACAAAGCAGTAAACCGAACATATGTCTTCAAG	1649
	CTTGAAGACATATGTTGCGTTTACTGCTTTGTCCAGATGAAC TCTTTGAGAATGAAAATGACTGTTTCTGTGATGAAGGAATATCT GTGGCATATTTTAAACTATAATCAATAGGCTGAT	1650
	GAAACAGTCATTTTCAT	1651
	ATGAAAATGACTGTTTC	1652
Adenomatous polyposis coli Ser1198Term TCA-TGA	ATTATAGTTTAAATATGCCACAGATATTCCTTCATCACAGAAA CAGTCATTTTCATTCTCAAAGAGTTCATCTGGACAAAGCAGTA AAACCGAACATATGTCTTCAAGCAGTGAGAATAC	1653
	GTATTCTCACTGCTTGAAGACATATGTTGCGTTTACTGCTTTG TCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGAT GAAGGAATATCTGTGGCATATTTTAAACTATAAT	1654
	TTCATTCTCAAAGAGTT	1655
	AACTCTTTGAGAATGAA	1656
Adenomatous polyposis coli Gln1228Term CAG-TAG	ACCGAACATATGTCTTCAAGCAGTGAGAATACGTCCACACCTT CATCTAATGCCAAGAGGCAGAATCAGCTCCATCCAGTTCTGC ACAGAGTAGAAGTGGTCAGCCTCAAAGGCTGCCACT	1657
	AGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGTGCAGAA CTGGATGGAGCTGATTCTGCCTCTTGGCATTAGATGAAGGTG TGGACGTATTCTCACTGCTTGAAGACATATGTTGCGT	1658
	CCAAGAGGCAGAATCAG	1659
	CTGATTCTGCCTCTTGG	1660

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Adenomatous polyposis coli Gln1230Term CAG-TAG	CATATGTCTTCAAGCAGTGAGAATACGTCCACACCTTCATCTA ATGCCAAGAGGCAGAATCAGCTCCATCCAGTTCTGCACAGAG TAGAAGTGGTCAGCCTCAAAGGCTGCCACTTGCAAG	1661
	CTTGCAAGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGT GCAGAACTGGATGGAGCTGATTCTGCCTCTTGGCATTAGATG AAGGTGTGGACGTATTCTCACTGCTTGAAGACATATG	1662
	GGCAGAATCAGCTCCAT	1663
	ATGGAGCTGATTCTGCC	1664
Adenomatous polyposis coli Cys1249Term TGC-TGA	TCAGCTCCATCCAAGTTCTGCACAGAGTAGAAGTGGTCAGCC TCAAAGGCTGCCACTTGCAAAGTTTCTTCTATTAACCAAGAA ACAATACAGACTTATTGTGTAGAAGATACTCCAATA	1665
	TATTGGAGTATCTTCTACACAATAAGTCTGTATTGTTTCTTGGT TAATAGAAGAACTTTGCAAGTGGCAGCCTTTTGGAGGCTGACC ACTTCTACTCTGTGCAGAACTTGGATGGAGCTGA	1666
	GCCACTTGCAAAGTTTC	1667
	GAAACTTTGCAAGTGGC	1668
Adenomatous polyposis coli Cys1270Term TGT-TGA	AGTTTCTTCTATTAACCAAGAAACAATACAGACTTATTGTGTAG AAGATACTCCAATATGTTTTCAAGATGTAGTTCATTATCATCT TTGTCATCAGCTGAAGATGAAATAGGATGTAAT	1669
	ATTACATCCTATTTTCATCTTCAGCTGATGACAAAGATGATAATG AACTACATCTTGAAAAACATATTGGAGTATCTTCTACACAATAA GTCTGTATTGTTTCTTGGTTAATAGAAGAACT	1670
	CCAATATGTTTTCAAG	1671
	CTTGAAAAACATATTGG	1672
Adenomatous polyposis coli Ser1276Term TCA-TGA	AAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATATGT TTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGAAGA TGAAATAGGATGTAATCAGACGACACAGGAAGC	1673
	GCTTCCTGTGTCGTCTGATTACATCCTATTTTCATCTTCAGCTG ATGACAAAGATGATAATGAACTACATCTTGAAAAACATATTGGA GTATCTTCTACACAATAAGTCTGTATTGTTTCTT	1674
	ATGTAGTTCATTATCAT	1675
	ATGATAATGAACTACAT	1676
Adenomatous polyposis coli Glu1286Term GAA-TAA	GATACTCCAATATGTTTTCAAGATGTAGTTCATTATCATCTTT GTCATCAGCTGAAGATGAAATAGGATGTAATCAGACGACACA GGAAGCAGATTCTGCTAATACCCTGCAAATAGCAG	1677
	CTGCTATTTGCAGGGTATTAGCAGAATCTGCTTCCTGTGTCGT CTGATTACATCCTATTTTCATCTTCAGCTGATGACAAAGATGATA ATGAACTACATCTTGAAAAACATATTGGAGTATC	1678
	CTGAAGATGAAATAGGA	1679
	TCCTATTTTCATCTTCAG	1680

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln1294Term CAG-TAG	TGTAGTTCATTATCATCTTTGTCATCAGCTGAAGATGAAATAGG ATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATACCCTG CAAATAGCAGAAATAAAAGAAAAGATTGGA ACTA	1681
	TAGTTCCAATCTTTTCTTTATTTCTGCTATTTGCAGGGTATTA GCAGAATCTGCTTCCTGTGTCGTCTGATTACATCCTATTTTCAT CTTCAGCTGATGACAAAGATGATAATGAACTACA	1682
	AGACGACACAGGAAGCA	1683
	TGCTTCCTGTGTCGTCT	1684
Predisposition to, association with, colorectal cancer Ile1307Lys ATA-AAA	TAGGATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATAC CCTGCAAATAGCAGAAATAAAAGAAAAGATTGGA ACTAGGTCA GCTGAAGATCCTGTGAGCGAAGTTCCAGCAGTGTC	1685
	GACACTGCTGGA ACTTCGCTCACAGGATCTTCAGCTGACCTA GTTCCAATCTTTTCTTTATTTCTGCTATTTGCAGGGTATTAGC AGAATCTGCTTCCTGTGTCGTCTGATTACATCCTA	1686
	AGCAGAAATAAAAGAAA	1687
	TTTCTTTTATTTCTGCT	1688
Adenomatous polyposis coli Glu1309Term GAA-TAA	CCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATA TGTTTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGA AGATGAAATAGGATGTAATCAGACGACACAGGAA	1689
	TTCCTGTGTCGTCTGATTACATCCTATTTTCATCTTCAGCTGATG ACAAAGATGATAATGAACTACATCTTGAAAACATATTGGAGTA TCTTCTACACAATAAGTCTGTATTGTTTCTTGG	1690
	AGATGTAGTTCATTATC	1691
	GATAATGAACTACATCT	1692
Predisposition to Colorectal Cancer Glu1317Gln GAA-CAA	GATTCTGCTAATACCCTGCAAATAGCAGAAATAAAAGAAAAGA TTGGA ACTAGGTCAGCTGAAGATCCTGTGAGCGAAGTTCCAG CAGTGTCACAGCACCCCTAGAACCAAATCCAGCAGAC	1693
	GTCTGCTGGATTTGGTTCTAGGGTGCTGTGACACTGCTGGAA CTTCGCTCACAGGATCTTCAGCTGACCTAGTTCCAATCTTTTC TTTTATTTCTGCTATTTGCAGGGTATTAGCAGAATC	1694
	GGTCAGCTGAAGATCCT	1695
	AGGATCTTCAGCTGACC	1696
Adenomatous polyposis coli Gln1328Term CAG-TAG	AAAGAAAAGATTGGA ACTAGGTCAGCTGAAGATCCTGTGAGC GAAGTTCCAGCAGTGTCACAGCACCCCTAGAACCAAATCCAGC AGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCA	1697
	TGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTGG ATTTGGTTCTAGGGTGCTGTGACACTGCTGGA ACTTCGCTCA CAGGATCTTCAGCTGACCTAGTTCCAATCTTTCTTT	1698
	CAGTGTCACAGCACCCCT	1699
	AGGGTGCTGTGACACTG	1700

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Adenomatous polyposis coli Gln1338Term CAG-TAG	GATCCTGTGAGCGAAGTTCAGCAGTGTACAGCACCCCTAGA ACCAAATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAAT CAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAG	1701
	CTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGA AGATAAACTAGAACCCTGCAGTCTGCTGGATTGTTCTAGG GTGCTGTGACACTGCTGGAACCTCGCTCACAGGATC	1702
	GCAGACTGCAGGGTTCT	1703
	AGAACCCTGCAGTCTGC	1704
Adenomatous polyposis coli Leu1342Term TTA-TAA	AAGTTCAGCAGTGTACAGCACCCCTAGAACCAAATCCAGCA GACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAA AGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTC	1705
	GAGGGAGATTTGCTCCTGAAGAAAATTCAACAGCTTTGTGC CTGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTG GATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACCTT	1706
	TTCTAGTTTATCTTCAG	1707
	CTGAAGATAAACTAGAA	1708
Adenomatous polyposis coli Arg1348Trp AGG-TGG	CAGCACCCCTAGAACCAAATCCAGCAGACTGCAGGGTTCTAGT TTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTTCTT CAGGAGCGAAATCTCCCTCCCGAAAGTGGTGCTCAG	1709
	CTGAGCACCCTTTGCGGGAGGGAGATTTGCTCCTGAAGAAA ATTCAACAGCTTTGTGCCTGGCTGATTCTGAAGATAAACTAGA ACCCTGCAGTCTGCTGGATTGTTCTAGGGTGCTG	1710
	AATCAGCCAGGCACAAA	1711
	TTTGTGCCTGGCTGATT	1712
Adenomatous polyposis coli Gly1357Term GGA-TGA	CTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAAG CTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCCGAAAGTG GTGCTCAGACACCCCAAAGTCCACCTGAACACTAT	1713
	ATAGTGTTGAGGTGGACTTTGGGGTGTCTGAGCACCCTTTC GGGAGGGAGATTTGCTCCTGAAGAAAATTCAACAGCTTTGT GCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAG	1714
	TTTCTTCAGGAGCGAAA	1715
	TTTCGCTCCTGAAGAAA	1716
Adenomatous polyposis coli Gln1367Term CAG-TAG	CCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCC CTCCCGAAAGTGGTGCTCAGACACCCCAAAGTCCACCTGAAC ACTATGTTGAGGAGACCCCACTCATGTTTAGCAGAT	1717
	ATCTGCTAACATGAGTGGGGTCTCCTGAACATAGTGTTGAG GTGGACTTTGGGGTGTCTGAGCACCCTTTCGGGAGGGAGAT TTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGG	1718
	GTGGTGCTCAGACACCC	1719
	GGGTGTCTGAGCACAC	1720

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Lys1370Term AAA-TAA	AAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCAAAA GTGGTGCTCAGACACCCAAAAGTCCACCTGAACACTATGTTC AGGAGACCCCACTCATGTTTAGCAGATGTACTTCTG	1721
	CAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAACATA GTGTTCAAGTGGACTTTTGGGTGTCTGAGCACCCTTTTGA GGGAGATTCGCTCCTGAAGAAAATTCAACAGCTTT	1722
	AGACACCCAAAAGTCCA	1723
	TGGACTTTTGGGTGTCT	1724
Adenomatous polyposis coli Ser1392Term TCA-TAA	CACCTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCA GATGTACTTCTGTCAGTTCACTTGATAGTTTTGAGAGTCGTTC GATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGG	1725
	CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGA CTCTCAAACTATCAAGTGAAGTGAACGACAGAAGTACATCTGCTAA ACATGAGTGGGGTCTCCTGAACATAGTGTTTCAGGTG	1726
	TGTCAGTTCACTTGATA	1727
	TATCAAGTGAAGTGAAC	1728
Adenomatous polyposis coli Ser1392Term TCA-TGA	CACCTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCA GATGTACTTCTGTCAGTTCACTTGATAGTTTTGAGAGTCGTTC GATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGG	1729
	CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGA CTCTCAAACTATCAAGTGAAGTGAACGACAGAAGTACATCTGCTAA ACATGAGTGGGGTCTCCTGAACATAGTGTTTCAGGTG	1730
	TGTCAGTTCACTTGATA	1731
	TATCAAGTGAAGTGAAC	1732
Adenomatous polyposis coli Glu1397Term GAG-TAG	GTTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCA GTTCACTTGATAGTTTTGAGAGTCGTTTCGATTGCCAGCTCCGT TCAGAGTGAACCATGCAGTGGAAATGGTAGGTGGCA	1733
	TGCCACCTACCATTCCACTGCATGGTTCACTCTGAACGGAGC TGGCAATCGAACGACTCTCAAACTATCAAGTGAAGTGAACGACAGA AGTACATCTGCTAAACATGAGTGGGGTCTCCTGAAC	1734
	ATAGTTTTGAGAGTCGT	1735
	ACGACTCTCAAACTAT	1736
Adenomatous polyposis coli Lys1449Term AAG-TAG	CAAACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCT CCTCAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAAG CACCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGC	1737
	GCTTAGGTCCACTCTCTCTCTTTTCAGCAGTAGGTGCTTTATT TTTAGGTACTTCTCGCTTGGTTTGAAGTGTGTTGAGGAGGTGGT GGAGGTGTTTTACTTCTGCTTGGTGGCATGGTTTG	1738
	CTCAAACCAAGCGAGAA	1739
	TTCTCGCTTGGTTTGAG	1740
Adenomatous polyposis coli Arg1450Term CGA-TGA	ACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCTCCT CAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAAGCAC CTACTGCTGAAAAGAGAGAGAGTGGACCTAAGCAAG	1741

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTGCTTAGGTCCACTCTCTCTTTTCAGCAGTAGGTGCTTT ATTTTATAGGTACTTCTCGCTTGGTTTGAGCTGTTTGAGGAGGT GGTGGAGGTGTTTACTTCTGCTTGGTGGCATGGT	1742
	AAACCAAGCGAGAAGTA	1743
	TACTTCTCGCTTGGTTT	1744
Adenomatous polyposis coli Ser1503Term TCA-TAA	CAGATGCTGATACTTTATTACATTTTGCCACGGAAAGTACTCC AGATGGATTTTCTTGTTATCCAGCCTGAGTGCTCTGAGCCTC GATGAGCCATTTATACAGAAAGATGTGGAATTAAG	1745
	CTTAATTCCACATCTTTCTGTATAAATGGCTCATCGAGGCTCA GAGCACTCAGGCTGGATGAACAAGAAAATCCATCTGGAGTAC TTCCGTGGCAAATGTAATAAAGTATCAGCATCTG	1746
	TTCTTGTTATCCAGCC	1747
	GGCTGGATGAACAAGAA	1748
Adenomatous polyposis coli Gln1529Term CAG-TAG	CTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAA GAATAATGCCTCCAGTTGAGGAAAATGACAATGGGAATGAAAC AGAATCAGAGCAGCCTAAAGAATCAAATGAAAACC	1749
	GGTTTTCAATTGATTCTTAGGCTGCTCTGATTCTGTTTCATTC CCATTGTCATTTTCCTGAACTGGAGGCATTATTCTTAATTCCAC ATCTTTCTGTATAAATGGCTCATCGAGGCTCAG	1750
	CTCCAGTTGAGGAAAAT	1751
	ATTTTCCTGAACTGGAG	1752
Adenomatous polyposis coli Ser1539Term TCA-TAA	ATGTGGAATTAAGAATAATGCCTCCAGTTGAGGAAAATGACAA TGGAATGAAACAGAATGAGAGCAGCCTAAAGAATCAAATGAA AACCAAGAGAAAGAGGCAGAAAAAACTATTGATTCT	1753
	GAATCAATAGTTTTTCTGCCTCTTTCTCTTGGTTTTCAATTGA TTCTTTAGGCTGCTCTGATTCTGTTTCATTCCCATTTGTCATTT CCTGAACTGGAGGCATTATTCTTAATTCCACAT	1754
	AACAGAATGAGAGCAGC	1755
	GCTGCTCTGATTCTGTT	1756
Adenomatous polyposis coli Ser1567Term TCA-TGA	AAAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTCTGAAAA GGACCTATTAGATGATTGAGATGATGATATTGAAATACTA GAAGAATGTATTATTTCTGCCATGCCAACAAAGTC	1757
	GACTTTGTTGGCATGGCAGAAATAACATTCTTAGTATTTT AATATCATCATCATCTGAATCATCTAATAGGTCCTTTTCAGAAT CAATAGTTTTTCTGCCTCTTTCTCTTGGTTTT	1758
	AGATGATTGAGATGATG	1759
	CATCATCTGAATCATCT	1760
Adenomatous polyposis coli Asp1822Val GAC-GTC	AGAGAGTTTTCTCAGACAACAAAGATTCAAAGAAACAGAATTT GAAAAATAATTCCAAGGACTTCAATGATAAGCTCCCAAATAAT GAAGATAGAGTCAGAGGAAGTTTTGCTTTTGATTCT	1761

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GAATCAAAAGCAA <u>A</u> CTTCCTCTGACTCTATCTTCATTATTTGG GAGCTTATCATTGAAGTCCTTGGAAATTATTTTCAAATTCTGT TCTTTGAATCTTTGTTGTCTGAGAAACTCTCT	1762
	TTCCAAGGACTTCAATG	1763
	CATTGAAGTCCTTGGAA	1764
Adenomatous polyposis coli Leu2839Phe CTT-TTT	AAA <u>A</u> CTGACAGCACAGAATCCAGTGGAACCCAAAGTCCTAAG CGCCATTCTGGGTCTTACCTTGTGACATCTGTTTAAAGAGAG GAAGAATGAACTAAGAAAATTCTATGTTAATTACA	1765
	TGTAATTAACATAGAATTTTCTTAGTTTCATTCTTCCTCTCTTTT AAACAGATGTCACAAGGTAAGACCCAGAATGGCGCTTAGGAC TTTGGGTTCCACTGGATTCTGTGCTGTCAGTTTT	1766
	GGTCTTACCTTGTGACA	1767
	TGTCACAAGGTAAGACC	1768

EXAMPLE 12

Parahemophilia - Factor V Deficiency

Deficiency in clotting Factor V is associated with a lifelong predisposition to thrombosis. The disease typically manifests itself with usually mild bleeding, although bleeding times and clotting times are consistently prolonged. Individuals that are heterozygous for a mutation in Factor V have lowered levels of factor V but probably never have abnormal bleeding. A large number of alleles with a range of presenting symptoms have been identified. The attached table discloses the correcting oligonucleotide base sequences for the Factor V oligonucleotides of the invention.

Table 19
Factor V Mutations and Genome-Correcting Oligos

[illegible]

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TGAAGTATTCCCACCTCTTCATGTGCCGCCTCTGCTCACGAGT TATTTTCTTAAGATTCC <u>TGG</u> TTTTCTTTGGGCAGTTTTTAATGT CAATGTAAGCCTGCATCCCAGCTGAGTTAGGACA	1773
	AGAAAACCAGGAATCTT	1774
	AAGATTCC <u>TGG</u> TTTTCT	1775
Thrombosis Arg306Thr AGG-ACG	GTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAA CTGCCCAAAGAAAACCAGGAATCTTAAGAAAATAACTCGTGAG CAGAGGCGGCACATGAAGAGGTGGGAATACTTCAT	1776
	ATGAAGTATTCCCACCTCTTCATGTGCCGCCTCTGCTCACGA GTTATTTTCTTAAGATTCC <u>TGG</u> TTTTCTTTGGGCAGTTTTTAAT GTCAATGTAAGCCTGCATCCCAGCTGAGTTAGGAC	1777
	GAAAACCAGGAATCTTA	1778
	TAAGATTCC <u>TGG</u> TTTTCT	1779
Increased Risk Thrombosis Arg485Lys AGA-AAA	CCACAGAAAATGATGCCCAGTGCTTAACAAGACCATACTACAG TGACGTGGACATCATGAGAGACATCGCCTCTGGGCTAATAGG ACTACTTCTAATCTGTAAGAGCAGATCCCTGGACAG	1780
	CTGTCCAGGGATCTGCTCTTACAGATTAGAAGTAGTCCTATTA GCCCAGAGGCGATGTCTCTCATGATGTCCACGTCACTGTAGT ATGGTCTTGTTAAGCACTGGGCATCATTTTCTGTGG	1781
	CATCATGAGAGACATCG	1782
	CGATGTCTCTCATGATG	1783
Increased Risk Thrombosis Arg506Gln CGA-CAA	ACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGAG CAGATCCCTGGACAGGCGAGGAATACAGGTATTTTGTCTTG AAGTAACCTTTAGAAATTCTGAGAATTTCTTCTGG	1784
	CCAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGAC AAAATACCTGTATTCCTCGCCTGTCCAGGGATCTGCTCTTACA GATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGT	1785
	GGACAGGCGAGGAATAC	1786
	GTATTCCTCGCCTGTCC	1787
Factor V Deficiency Arg506Term CGA-TGA	GACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGA GCAGATCCCTGGACAGGCGAGGAATACAGGTATTTTGTCTTG GAAGTAACCTTTAGAAATTCTGAGAATTTCTTCTG	1788
	CAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGACA AAATACCTGTATTCCTCGCCTGTCCAGGGATCTGCTCTTACAG ATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGTC	1789
	TGGACAGGCGAGGAATA	1790
	TATTCCTCGCCTGTCCA	1791
Thrombosis Arg712Term CGA-TGA	AGTGATGCTGACTATGATTACCAGAACAGACTGGCTGCAGCA TTAGGAATCAGGTCATTCCGAAACTCATCATTGAATCAGGAAG AAGAAGAGTTCAATCTTACTGCCCTAGCTCTGGAGA	1792
	TCTCCAGAGCTAGGGCAGTAAGATTGAACTCTTCTTCTTCTG ATTCAATGATGAGTTTCGGAATGACCTGATTCCTAATGCTGCA GCCAGTCTGTTCTGGTAATCATAGTCAGCATCACT	1793
	GGTCATTCCGAAACTCA	1794

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGAGTTTCGGAATGACC	1795
Thrombosis His1299Arg CAT-CGT	TCAGTCAGACAAACCTTTCCCCAGCCCTCGGTCAGATGCCCA TTTCTCCAGACCTCAGCCATACAACCCTTTCTCTAGACTTCAG CCAGACAAACCTCTCTCCAGAACTCAGTCAAACAAA	1796
	TTTGTTTGACTGAGTTCTGGAGAGAGGTTTGTCTGGCTGAAGT CTAGAGAAAGGGTTGTA ^T GGCTGAGGTCTGGAGAAATGGGCA TCTGACCGAGGGCTGGGGAAAGGTTTGTCTGACTGA	1797
	CCTCAGCCATACAACCC	1798
	GGGTTGTATGGCTGAGG	1799

EXAMPLE 13
Hemophilia - Factor VIII Deficiency

The attached table discloses the correcting oligonucleotide base sequences for the Factor VIII oligonucleotides of the invention.

Table 20
Factor VIII Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Tyr5Cys TAC-TGC	AGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTT TAGTGCCACCAGAAGATA ^T CTACCTGGGTGCAGTGGAAGTGC ATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCC	1800
	GGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGT TCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAG AATCGCAAAAGGCACAGAAAGAAGCAGGTGGAGAGCT	1801
	CAGAAGATA ^T CTACCTGG	1802
	CCAGGTAGTATCTTCTG	1803
Haemophilia A Leu7Arg CTG-CGG	CCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTTTAGTGC CACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTGATGGGA CTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGA	1804
	TCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCAT GACAGTTCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTA AAGCAGAATCGCAAAAGGCACAGAAAGAAGCAGGTGG	1805
	ATACTACCTGGGTGCAG	1806
	CTGCACCCAGGTAGTAT	1807
Haemophilia A Ser(-1)Arg AGTg-AGG	AGTCATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTT TTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGGT GCAGTGGAAGTGTGATGGGACTATATGCAAAGTGAT	1808

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAG GTAGTATCTTCTGGTGGCACTAAAGCAGAATCGCAAAGGCA CAGAAAGAAGCAGGTGGAGAGCTCTATTTGCATGACT	1809
	TGCTTTAGTGCCACCAG	1810
	CTGGTGGCACTAAAGCA	1811
Haemophilia A Arg(-5)Term gCGA-TGA	CATTTGTAGCAATAAGTCATGCAAATAGAGCTCTCCACCTGCT TCTTTCTGTGCCTTTTGCGATTCTGCTTTAGTGCCACCAGAAG ATACTACCTGGGTGCAGTGGAACTGTCATGGGACT	1812
	AGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGG TGGCACTAAAGCAGAATCGCAAAGGACAGAAAGAAGCAGG TGGAGAGCTCTATTTGCATGACTTATTGCTACAAATG	1813
	GCCTTTTGCGATTCTGC	1814
	GCAGAATCGCAAAGGC	1815
Haemophilia A Glu11Val GAA-GTA	TTCTGTGCCTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATA CTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAG TGATCTCGGTGAGCTGCCTGTGGACGCAAGGTAAAG	1816
	CTTTACCTTGCGTCCACAGGCAGCTCACCGAGATCACTTTGC ATATAGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTC TGGTGGCACTAAAGCAGAATCGCAAAGGACAGAA	1817
	TGCAGTGGAACTGTCAT	1818
	ATGACAGTTCCACTGCA	1819
Haemophilia A Trp14Gly aTGG-GGG	CTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACCTGG GTGCACTGGAACTGTCATGGGACTATATGCAAAGTGATCTCG GTGAGCTGCCTGTGGACGCAAGGTAAAGGCATGTCC	1820
	GGACATGCCTTTACCTTGCGTCCACAGGCAGCTCACCGAGAT CACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGGT AGTATCTTCTGGTGGCACTAAAGCAGAATCGCAAAG	1821
	AACTGTCACTGGGACTAT	1822
	ATAGTCCCATGACAGTT	1823
Haemophilia A Tyr46Term TACa-TAA	TTCACGCAGATTTCTCCTAGAGTGCCAAAATCTTTCCATTC AACACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCA CGGATCACCTTTTCAACATCGCTAAGCCAAGGCCA	1824
	TGGCCTTGGCTTAGCGATGTTGAAAAGGTGATCCGTGAATTC TACAAACAGAGTCTTTTGTACACGACTGAGGTGTTGAATGGA AAAGATTTTGGCACTCTAGGAGGAAATCTGCGTGAA	1825
	GTCGTGTACAAAAAGAC	1826
	GTCTTTTGTACACGAC	1827
Haemophilia A Asp56Glu GATc-GAA	ATCTTTTCCATTCAACACCTCAGTCGTGTACAAAAGACTCTG TTTGTAGAATTCACGGAACACCTTTTCAACATCGCTAAGCCAA GGCCACCCTGGATGGGTAATGAAAACAATGTTGAA	1828

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTCAACATTGTTTTATTACCCATCCAGGGTGGCCTTGGCTTA GCGATGTTGAAAAGGTGATCCGTGAATTCTACAAACAGAGTC TTTTTGTACACGACTGAGGTGTTGAATGGAAAAGAT	1829
	TTCACGGATCACCTTTT	1830
	AAAAGGTGATCCGTGAA	1831
Haemophilia A Gly73Val GGT-GTT	TTCTGGAGTACTATCCCCAAGTAACCTTTGGCGGACATCTCAT TCTTACAGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA TGATACAGTGGTCATTACACTTAAGAACATGGCTTC	1832
	GAAGCCATGTTCTTAAGTGTAATGACCACTGTATCATAAACCT CAGCCTGGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT GTCCGCCAAAGGTTACTTGGGGATAGTACTCCAGAA	1833
	TCTGCTAGGTCCTACCA	1834
	TGGTAGGACCTAGCAGA	1835
Haemophilia A Glu79Lys tGAG-AAG	CAAGTAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAG GTCCTACCATCCAGGCTGAGGTTATGATACAGTGGTCATTAC ACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTC	1836
	GAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAATGA CCTGTATCATAAACCTCAGCCTGGATGGTAGGACCTAGCA GACCTGTAAGAATGAGATGTCCGCCAAAGGTTACTTG	1837
	TCCAGGCTGAGGTTTAT	1838
	ATAAACCTCAGCCTGGA	1839
Haemophilia A Val80Asp GTT-GAT	TAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCC TACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACTT AAGAACATGGCTTCCCATCCTGTCAGTCTTCATGC	1840
	GCATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTA ATGACCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCT AGCAGACCTGTAAGAATGAGATGTCCGCCAAAGGTTA	1841
	GGCTGAGGTTTATGATA	1842
	TATCATAAACCTCAGCC	1843
Haemophilia A Asp82Val GAT-GTT	TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAAC ATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG	1844
	CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA	1845
	GGTTTATGATACAGTGG	1846
	CCACTGTATCATAAACC	1847
Haemophilia A Asp82Gly GAT-GGT	TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAAC ATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG	1848

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA	1849
	GGTTTATGATACAGTGG	1850
	CCACTGTATCATAAAC	1851
Haemophilia A Val85Asp GTC-GAC	ATCTCATTCTTACAGGTCTGCTAGGTCCTACCATCCAGGCTGA GGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCC CATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTA	1852
	TAGGATACACCAACAGCATGAAGACTGACAGGATGGGAAGCC ATGTTCTTAAGTGTAAATGACCACTGTATCATAAACCTCAGCCT GGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT	1853
	TACAGTGGTCATTACAC	1854
	GTGTAATGACCACTGTA	1855
Haemophilia A Lys89Thr AAG-ACG	CAGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATA CAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCA GTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTC	1856
	GAAGCTTTCAGTAGGATACACCAACAGCATGAAGACTGACA GGATGGGAAGCCATGTTCTTAAGTGTAAATGACCACTGTATCAT AACCTCAGCCTGGATGGTAGGACCTAGCAGACCTG	1857
	TACACTTAAGAACATGG	1858
	CCATGTTCTTAAGTGTAA	1859
Haemophilia A Met91Val cATG-GTG	CTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTG GTCATTACACTTAAGAACATGGCTTCCCATCCTGTCACTTTC ATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGAGG	1860
	CCTCAGAAGCTTTCAGTAGGATACACCAACAGCATGAAGAC TGACAGGATGGGAAGCCATGTTCTTAAGTGTAAATGACCACTG TATCATAAACCTCAGCCTGGATGGTAGGACCTAGCAG	1861
	TTAAGAACATGGCTTCC	1862
	GGAAGCCATGTTCTTAA	1863
Haemophilia A His94Arg CAT-CGT	CTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACT TAAGAACATGGCTTCCCATCCTGTCACTTTCATGCTGTTGGT GTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAA	1864
	TTTTACTCACCCTCAGAAGCTTTCAGTAGGATACACCAACAG CATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA TGACCACTGTATCATAAACCTCAGCCTGGATGGTAG	1865
	GGCTTCCCATCCTGTCA	1866
	TGACAGGATGGGAAGCC	1867
Haemophilia A His94Tyr cCAT-TAT	CCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACAC TTAAGAACATGGCTTCCCATCCTGTCACTTTCATGCTGTTGG TGTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAA	1868

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTTACTCACCTCAGAAGCTTTCCAGTAGGATACACCAACAGC ATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAAT GACCACTGTATCATAAACCTCAGCCTGGATGGTAGG	1869
	TGGCTTCCCATCCTGTC	1870
	GACAGGATGGGAAGCCA	1871
Haemophilia A Leu98Arg CTT-CGT	CTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGC TTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGG AAAGCTTCTGAGGGTGAGTAAATACCCTCCTATT	1872
	AATAGGAGGGTATTTTACTCACCTCAGAAGCTTTCCAGTAGG ATACACCAACAGCATGAAGACTGACAGGATGGGAAGCCATGT TCTTAAGTGTAATGACCACTGTATCATAAACCTCAG	1873
	TGTCAGTCTTCATGCTG	1874
	CAGCATGAAGACTGACA	1875
Haemophilia A Gly102Ser tGGT-AGT	GATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTG TCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGA GGGTGAGTAAATACCCTCCTATTGTCCTGTCATT	1876
	AATGACAGGACAATAGGAGGGTATTTTACTCACCTCAGAAG CTTTCCAGTAGGATACACCAACAGCATGAAGACTGACAGGAT GGGAAGCCATGTTCTTAAGTGTAATGACCACTGTATC	1877
	ATGCTGTTGGTGTATCC	1878
	GGATACACCAACAGCAT	1879
Haemophilia A Glu113Asp GAAT-GAC	CTTTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTTC CTGCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGGG AGAAAGAAGATGATAAAGTCTTCCCTGGTGGGAAGC	1880
	GCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGA CTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAATA AAATTGTCCTTTCTATATCCACTGTACACTCAAAG	1881
	GGAGCTGAATATGATGA	1882
	TCATCATATTCAGCTCC	1883
Haemophilia A Tyr114Cys TAT-TGT	TTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTTCCT GCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAG AAAGAAGATGATAAAGTCTTCCCTGGTGGGAAGCCA	1884
	TGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT GACTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAA TAAATTGTCCTTTCTATATCCACTGTACACTCAA	1885
	AGCTGAATATGATGATC	1886
	GATCATCATATTCAGCT	1887
Haemophilia A Asp116Gly GAT-GGT	GTACAGTGGATATAGAAAGGACAATTTTATTTCTTCCTGCTATA GGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAA GATGATAAAGTCTTCCCTGGTGGGAAGCCATACATA	1888

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCT CCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATAGCAGG AAGAAATAAAATTGTCCTTTCTATATCCACTGTAC	1889
	ATATGATGATCAGACCA	1890
	TGGTCTGATCATCATAT	1891
Haemophilia A Gln117Term tCAG-TAG	ACAGTGGATATAGAAAGGACAATTTTATTTCTTCCTGCTATAG GAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAAG ATGATAAAGTCTTCCCTGGTGAAGCCATACATATG	1892
	CATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTT CTCCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATAGCA GGAAGAAATAAAATTGTCCTTTCTATATCCACTGT	1893
	ATGATGATCAGACCAGT	1894
	ACTGGTCTGATCATCAT	1895
Haemophilia A Thr118Ile ACC-ATC	TGGATATAGAAAGGACAATTTTATTTCTTCCTGCTATAGGAGC TGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAAGATGA TAAAGTCTTCCCTGGTGAAGCCATACATATGTCTG	1896
	CAGACATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTT CTTTCTCCCTTTGACTGGTCTGATCATCATATTCAGCTCCTAT AGCAGGAAGAAATAAAATTGTCCTTTCTATATCCA	1897
	TGATCAGACCAGTCAAA	1898
	TTTGACTGGTCTGATCA	1899
Haemophilia A Glu122Term gGAG-TAG	AGGACAATTTTATTTCTTCCTGCTATAGGAGCTGAATATGATG ATCAGACCAGTCAAAGGGAGAAAGAAGATGATAAAGTCTTCC CTGGTGAAGCCATACATATGTCTGGCAGGTCCTGA	1900
	TCAGGACCTGCCAGACATATGTATGGCTTCCACCAGGGAAGA CTTTATCATCTTCTTTCTCCCTTTGACTGGTCTGATCATCATAT TCAGCTCCTATAGCAGGAAGAAATAAAATTGTCCT	1901
	GTCAAAGGGAGAAAGAA	1902
	TTCTTTCTCCCTTTGAC	1903
Haemophilia A Asp126His tGAT-CAT	TTTCTTCCTGCTATAGGAGCTGAATATGATGATCAGACCAGTC AAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGAAGCC ATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTC	1904
	GACCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTTCC ACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGACTGGTC TGATCATCATATTCAGCTCCTATAGCAGGAAGAAA	1905
	AAGAAGATGATAAAGTC	1906
	GACTTTATCATCTTCTT	1907
Haemophilia A Gln139Term gCAG-TAG	AGTCAAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGA AGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCA ATGGCCTCTGACCCACTGTGCCTTACCTACTCATATC	1908

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGA CCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTTCCAC CAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGACT	1909
	ATGTCTGGCAGGTCCTG	1910
	CAGGACCTGCCAGACAT	1911
Haemophilia A Val140Ala GTC-GCC	AAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGG CCTCTGACCCACTGTGCCTTACCTACTCATATCTTTC	1912
	GAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATT GGACCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTT CCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT	1913
	CTGGCAGGTCCTGAAAG	1914
	CTTTCAGGACCTGCCAG	1915
Haemophilia A Asn144Lys AATg-AAA	AGATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTG GCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACT GTGCCTTACCTACTCATATCTTCTCATGTGGACCTG	1916
	CAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGG GTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCCAGAC ATATGTATGGCTTCCACCAGGGAAGACTTTATCATCT	1917
	AAAGAGAATGGTCCAAT	1918
	ATTGGACCATTCTCTT	1919
Haemophilia AG Gly145Asp GGT-GAT	ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCA GGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTG CCTTACCTACTCATATCTTCTCATGTGGACCTGGT	1920
	ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT	1921
	AGAGAATGGTCCAATGG	1922
	CCATTGGACCATTCTCT	1923
Haemophilia A Gly145Val GGT-GTT	ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCA GGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTG CCTTACCTACTCATATCTTCTCATGTGGACCTGGT	1924
	ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT	1925
	AGAGAATGGTCCAATGG	1926
	CCATTGGACCATTCTCT	1927
Haemophilia A Pro146Ser tCCA-TCA	GATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAG GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTTCTCATGTGGACCTGGTAA	1928

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACA GTGGGTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCC AGACATATGTATGGCTTCCACCAGGGAAGACTTTATC	1929
	AGAATGGTCCAATGGCC	1930
	GGCCATTGGACCATTCT	1931
Haemophilia A Cys153Trp TGCC-TGG	CCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAAT GGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCAT GTGGACCTGGTAAAAGACTTGAATTCAGGCCTCATT	1932
	AATGAGGCCTGAATTCAAGTCTTTTACCAGGTCCACATGAGAA AGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGA CCATTCTCTTTCAGGACCTGCCAGACATATGTATGG	1933
	CCACTGTGCCTTACCTA	1934
	TAGGTAAGGCACAGTGG	1935
Haemophilia A Tyr156Term TACt-TAA	TGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGA CCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTG GTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTA	1936
	TAGGGCTCCAATGAGGCCTGAATTCAAGTCTTTTACCAGGTC CACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGA GGCCATTGGACCATTCTCTTTCAGGACCTGCCAGACA	1937
	CTTACCTACTCATATCT	1938
	AGATATGAGTAGGTAAG	1939
Haemophilia A Ser157Pro cTCA-CCA	GTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGAC CCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGG TAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTAC	1940
	GTAGGGCTCCAATGAGGCCTGAATTCAAGTCTTTTACCAGGT CCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAG AGGCCATTGGACCATTCTCTTTCAGGACCTGCCAGAC	1941
	TTACCTACTCATATCTT	1942
	AAGATATGAGTAGGTAA	1943
Haemophilia A Ser160Pro tTCT-CCT	GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTTICTCATGTGGACCTGGTAAAAGACT TGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTA	1944
	TACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAAGTCTTT TACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAG TGGGTCAGAGGCCATTGGACCATTCTCTTTCAGGAC	1945
	CATATCTTICTCATGTG	1946
	CACATGAGAAAGATATG	1947
Haemophilia A Val162Met tGTG-ATG	AAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACC TACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATT CAGGCCTCATTGGAGCCCTACTAGTATGTAGAGAAG	1948

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTCTCTACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAA GTCTTTTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAG GCACAGTGGGTCAGAGGCCATTGGACCATTCTCTTT	1949
	TTTCTCATGTGGACCTG	1950
	CAGGTCCACATGAGAAA	1951
Haemophilia A Lys166Thr AAA-ACA	CAATGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTC TCATGTGGACCTGGTAAAGACTTGAATTCAGGCCTCATTGG AGCCCTACTAGTATGTAGAGAAGGTAAGTGTATGAA	1952
	TTCATACACTTACCTTCTCTACATACTAGTAGGGCTCCAATGA GGCCTGAATTCAAGTCTTTTACCAGGTCCACATGAGAAAGATA TGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTG	1953
	CCTGGTAAAGACTTGA	1954
	TCAAGTCTTTTACCAGG	1955
Haemophilia A Ser170Leu TCA-TTA	ACCCACTGTGCCTTACCTACTCATATCTTCTCATGTGGACCT GGTAAAGACTTGAATTCAGGCCTCATTGGAGCCCTACTAGT ATGTAGAGAAGGTAAGTGTATGAAAGCGTAGGATTG	1956
	CAATCCTACGCTTTCATACACTTACCTTCTCTACATACTAGTAG GGCTCCAATGAGGCCTGAATTCAAGTCTTTTACCAGGTCCAC ATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGT	1957
	CTTGAATTCAGGCCTCA	1958
	TGAGGCCTGAATTCAAG	1959
Haemophilia A Phe195Val aTTT-GTT	AATGTTCTCACTTCTTTTTTCAGGGAGTCTGGCCAAGGAAAAGA CACAGACCTTGCACAAATTATACTACTTTTTGCTGTATTTGAT GAAGGTTAGTGAGTCTTAATCTGAATTTTGGATT	1960
	AATCCAAAATTCAGATTAAGACTCACTAACCTTCATCAAATACA GCAAAAAGTAGTATAAATTTGTGCAAGGTCTGTGTCTTTTCCT TGGCCAGACTCCCTGAAAAGAAGTGAGAACATT	1961
	TGCACAAATTTATACTA	1962
	TAGTATAAATTTGTGCA	1963
Haemophilia A Leu198His CTT-CAT	CTTCTTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCT TGCACAAATTTATACTACTTTTTGCTGTATTTGATGAAGGTTAG TGAGTCTTAATCTGAATTTTGGATTCCTGAAAGAA	1964
	TTCTTTCAGGAATCCAAAATTCAGATTAAGACTCACTAACCTTC ATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAGGTCTGT GTCTTTTCCTTGGCCAGACTCCCTGAAAAGAAG	1965
	TATACTACTTTTTGCTG	1966
	CAGCAAAAAGTAGTATA	1967
Haemophilia A Ala200Asp GCT-GAT	TTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCACA AATTTATACTACTTTTTGCTGTATTTGATGAAGGTTAGTGAGTC TTAATCTGAATTTTGGATTCCTGAAAGAAATCCTC	1968

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGGATTTCTTTCAGGAATCCAAAATTCAGATTAAGACTCACT AACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAA GGTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAA	1969
	ACTTTTGTCTGTATTTG	1970
	CAAATACAGCAAAAAGT	1971
Haemophilia A Ala200Thr tGCT-ACT	TTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCAC AAATTTATACTACTTTTGTCTGTATTTGATGAAGGTAGTGAGT CTTAATCTGAATTTTGGATTCTGAAAGAAATCCT	1972
	AGGATTTCTTTCAGGAATCCAAAATTCAGATTAAGACTCACTA ACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAG GTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAAA	1973
	TACTTTTGTCTGTATTT	1974
	AAATACAGCAAAAAGTA	1975
Haemophilia A Val234Phe aGTC-TTC	AACTCCTTGATGCAGGATAGGGATGCTGCATCTGCTCGGGCC TGGCCTAAATGCACACAGTCAATGGTTATGTAAACAGGTCTC TGCCAGGTATGTACACACCTGCTCAACAATCCTCAG	1976
	CTGAGGATTGTTGAGCAGGTGTGTACATACCTGGCAGAGACC TGTTTACATAACCAATTGACTGTGTGCATTTTAGGCCAGGCCCG AGCAGATGCAGCATCCCTATCCTGCATCAAGGAGTT	1977
	TGCACACAGTCAATGGT	1978
	ACCATTGACTGTGTGCA	1979
Haemophilia A Gly247Glu GGA-GAA	ATTTACAGATTCTCTACTTCATAGCCATAGGTGTCTTATTCCTAC TTTACAGGTCTGATTGGATGCCACAGGAAATCAGTCTATTGGC ATGTGATTGGAATGGGCACCACTCCTGAAGTGCA	1980
	TGCACTTCAGGAGTGGTGCCCATTCGAATCACATGCCAATAG ACTGATTTCTGTGGCATCCAATCAGACCTGTAAAGTAGGAAT AAGACACCTATGGCTATGAAGTAGAGAATCTGAAAT	1981
	TCTGATTGGATGCCACA	1982
Haemophilia A Trp255Cys TGGc-TGT	TGTGGCATCCAATCAGA	1983
	ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA	1984
	TGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT GCCCATTCGAATCACATGCCAATAGACTGATTTCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT	1985
	GTCTATTGGCATGTGAT	1986
Haemophilia A Trp255Term TGGc-TGA	ATCACATGCCAATAGAC	1987
	ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA	1988

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGGT GCCCATTCGAATCACATGCCAATAGACTGATTTCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT	1989
	GTCTATTGGCATGTGAT	1990
	ATCACATGCCAATAGAC	1991
Haemophilia A His256Leu CAT-CTT	AGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCACAG GAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCC TGAAGTGCACCTCAATATTCCTCGAAGGTCACACATT	1992
	AATGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTG GTGCCCATTCCAATCACATGCCAATAGACTGATTTCTGTGG CATCCAATCAGACCTGTAAAGTAGGAATAAGACACCT	1993
	CTATTGGCATGTGATTG	1994
	CAATCACATGCCAATAG	1995
Haemophilia A Gly259Arg tGGA-AGA	TATTCCTACTTTACAGGTCTGATTGGATGCCACAGGAAATCAG TCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAGTGC ACTCAATATTCCTCGAAGGTCACACATTTCTTGTGA	1996
	TCACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACCTC AGGAGTGGTGCCCATTCGAATCACATGCCAATAGACTGATTT CCTGTGGCATCCAATCAGACCTGTAAAGTAGGAATA	1997
	ATGTGATTGGAATGGGC	1998
	GCCCATTCGAATCACAT	1999
Haemophilia A Val266Gly GTG-GGG	TTGGATGCCACAGGAAATCAGTCTATTGGCATGTGATTGGAAT GGGCACCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTCA CACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTT	2000
	AAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCT TCGAGGAATATTGAGTGCACCTTCAGGAGTGGTGCCCATTCGA ATCACATGCCAATAGACTGATTTCTGTGGCATCCAA	2001
	TCCTGAAGTGCACCTCAA	2002
	TTGAGTGCACCTTCAGGA	2003
Haemophilia A Glu272Gly GAA-GGA	CAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAG TGCACTCAATATTCCTCGAAGGTACACATTTCTTGTGAGGAA CCATCGCCAGGCGTCCTTGGAATCTCGCCAATAAC	2004
	GTTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTC ACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACCTCAG GAGTGGTGCCCATTCGAATCACATGCCAATAGACTG	2005
	ATTCCTCGAAGGTCACA	2006
	TGTGACCTTCGAGGAAT	2007
Haemophilia A Glu272Lys cGAA-AAA	TCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA GTGCACTCAATATTCCTCGAAGGTACACATTTCTTGTGAGGA ACCATCGCCAGGCGTCCTTGGAATCTCGCCAATAA	2008

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCA CAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAG GAGTGGTGCCCATTCCAATCACATGCCAATAGACTGA	2009
	TATTCCTCGAAGGTCAC	2010
	GTGACCTTCGAGGAATA	2011
Haemophilia A Thr275Ile ACA-ATA	GGCATGTGATTGGAATGGGCACCACTCCTGAAGTGCACTCAA TATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGGAATCTCGCCAATAACTTTCTTAC	2012
	GTAAGGAAAGTTATTGGCGAGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAATGTGTGACCTTCGAGGAATATTGAGT GCACTTCAGGAGTGGTGCCCATTCCAATCACATGCC	2013
	AGGTCACACATTTCTTG	2014
	CAAGAAATGTGTGACCT	2015
Haemophilia A Val278Ala GTG-GCG	TTGGAATGGGCACCACTCCTGAAGTGCACTCAATATTCCTCG AAGGTCACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCT TGGAATCTCGCCAATAACTTTCTTACTGCTCAAAC	2016
	GTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCCAAGGAC GCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCTTCGAGG AATATTGAGTGCACTTCAGGAGTGGTGCCCATTCCAA	2017
	ATTTCTTGTGAGGAACC	2018
	GGTTCCTCACAAGAAAT	2019
Haemophilia A Asn280Ile AAC-ATC	TGGGCACCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTC ACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGAAA TCTCGCCAATAACTTTCTTACTGCTCAAACACTCTT	2020
	AAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCCA AGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCTT CGAGGAATATTGAGTGCACTTCAGGAGTGGTGCCCA	2021
	TGTGAGGAACCATCGCC	2022
	GGCGATGGTTCCTCACA	2023
Haemophilia A Arg282Cys tCGC-TGC	ACCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACAT TTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCTCGC CAATAACTTTCTTACTGCTCAAACACTCTTGATGG	2024
	CCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGA TTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGT GACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT	2025
	GGAACCATCGCCAGGCG	2026
	CGCCTGGCGATGGTTCC	2027
Haemophilia A Arg282His CGC-CAC	CCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCTCGCC AATAACTTTCTTACTGCTCAAACACTCTTGATGGA	2028

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGG	2029
	GAACCATCGCCAGGCGT	2030
	ACGCCTGGCGATGGTTC	2031
Haemophilia A Arg282Leu CGC-CTC	CCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGCC AATAACTTTCTTACTGCTCAAACACTCTTGATGGA	2032
	TCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGG	2033
	GAACCATCGCCAGGCGT	2034
	ACGCCTGGCGATGGTTC	2035
Haemophilia A Ala284Glu GCG-GAG	CTGAAGTGCACTCAATATTCCTCGAAGGTCACACATTTCTTC GAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGCCAATAA TTTCCTTACTGCTCAAACACTCTTGATGGACCTTGG	2036
	CCAAGGTCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATT GGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAG AAATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAG	2037
	TCGCCAGGCGTCCTTGG	2038
	CCAAGGACGCCTGGCGA	2039
Haemophilia A Ala284Pro gGCG-CCG	CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATTTCTTG TGAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGCCAATAA CTTTCCTTACTGCTCAAACACTCTTGATGGACCTTG	2040
	CAAGGTCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTG GCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAA ATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGG	2041
	ATCGCCAGGCGTCCTTG	2042
	CAAGGACGCCTGGCGAT	2043
Haemophilia A Ser289Leu TCG-TTG	TATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGGAAATCTCGCCAATAACTTTCTTACTGCTCAA AACTCTTGATGGACCTTGGACAGTTTCTACTGTT	2044
	AACAGTAGAACTGTCCAAGGTCCATCAAGAGTGTTTGAGCA GTAAGGAAAGTTATTGGCGAGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAATGTGTGACCTTCGAGGAATA	2045
	GGAAATCTCGCCAATAA	2046
	TTATTGGCGAGATTTCC	2047
Haemophilia A Phe293Ser TTC-TCC	GTCACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGG AAATCTCGCCAATAACTTTCTTACTGCTCAAACACTCTTGAT GGACCTTGGACAGTTTCTACTGTTTGTGTCATATCTC	2048

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGATATGACAAAACAGTAGAACTGTCCAAGGTCCATCAAG AGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTCCAAG GACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGAC	2049
	AATAACTTTCCTTACTG	2050
	CAGTAAGGAAAGTTATT	2051
		2052
Haemophilia A Thr295Ala TACT-GCT	ACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATC TCGCCAATAACTTTCTTACTGCTCAAACACTCTTGATGGACC TTGGACAGTTTCTACTGTTTTGTCATATCTCTTCCC	2053
	GGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGGTCCA TCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTC CAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGT	2054
	CTTTCCTTACTGCTCAA	2055
	TTGAGCAGTAAGGAAAG	2056
Haemophilia A Thr295Ile ACT-ATT	CATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCT CGCCAATAACTTTCTTACTGCTCAAACACTCTTGATGGACCT TGGACAGTTTCTACTGTTTTGTCATATCTCTTCCCA	2057
	TGGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGGTCC ATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGATT CCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATG	2058
	TTTCCTTACTGCTCAA	2059
	TTTGAGCAGTAAGGAAA	2060
Haemophilia A Ala296Val GCT-GTT	TTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCTCGC CAATAACTTTCTTACTGCTCAAACACTCTTGATGGACCTTGG ACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCA	2061
	TGGTGGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGG TCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAA	2062
	CCTTACTGCTCAAACAC	2063
	GTGTTTGAGCAGTAAGG	2064
Haemophilia A Leu308Pro CTG-CCG	TCTCGCCAATAACTTTCTTACTGCTCAAACACTCTTGATGGA CCTTGGACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCAA CATGGTAATATCTTGGATCTTTAAATGAATATTA	2065
	TAATATTCATTTTAAAGATCCAAGATATTACCATGTTGGTGGGA AGAGATATGACAAAACAGTAGAACTGTCCAAGGTCCATCAA GAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGA	2066
	GTTTCTACTGTTTTGTC	2067
	GACAAAACAGTAGAAAC	2068
Haemophilia A Glu321Lys gGAA-AAA	ACAGCCTAATATAGCAAGACACTCTGACATTGTTTGGTTTGTG TGA CTCCAGATGGCATGGAAGCTTATGTCAAAGTAGACAGCT GTCCAGAGGAACCCCACTACGAATGAAAAATAATG	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATTATTTTTCATTCTAGTTGGGGTTCCTCTGGACAGCTGTC TACTTTGACATAAGCTTCCATGCCATCTGGAGTCAGACAAACC AAACAATGTCAGAGTGTCTTGCTATATTAGGCTGT	2069
	ATGGCATGGAAGCTTAT	2070
	ATAAGCTTCCATGCCAT	2071
Haemophilia A Tyr323Term TATg-TAA	ATATAGCAAGACACTCTGACATTGTTTGGTTTGTCTGACTCCA GATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGTCCAGAG GAACCCCAACTACGAATGAAAAATAATGAAGAAGCG	2072
	CGCTTCTTCATTATTTTTCATTCTAGTTGGGGTTCCTCTGGA CAGCTGTCTACTTTGACATAAGCTTCCATGCCATCTGGAGTCA GACAAACCAACAATGTCAGAGTGTCTTGCTATAT	2073
	GAAGCTTATGTCAAAGT	2074
	ACTTTGACATAAGCTTC	2075
Haemophilia A Val326Leu aGTA-CTA	AAGACACTCTGACATTGTTTGGTTTGTCTGACTCCAGATGGCA TGGAAGCTTATGTCAAAGTAGACAGCTGTCCAGAGGAACCCC AACTACGAATGAAAAATAATGAAGAAGCGGAAGACT	2076
	AGTCTTCCGCTTCTTCATTATTTTTCATTCTAGTTGGGGTTC CTCTGGACAGCTGTCTACTTTGACATAAGCTTCCATGCCATCT GGAGTCAGACAAACCAACAATGTCAGAGTGTCTT	2077
	ATGTCAAAGTAGACAGC	2078
	GCTGTCTACTTTGACAT	2079
Haemophilia A Cys329Arg cTGT-CGT	TGACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTT ATGTCAAAGTAGACAGCTGTCCAGAGGAACCCCAACTACGAA TGAAAAATAATGAAGAAGCGGAAGACTATGATGATG	2080
	CATCATCATAGTCTTCCGCTTCTTCATTATTTTTCATTCTAGT TGGGGTTCCTCTGGACAGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAACAATGTCA	2081
	TAGACAGCTGTCCAGAG	2082
	CTCTGGACAGCTGTCTA	2083
Haemophilia A Cys329Tyr TGT-TAT	GACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTTA TGTCAAAGTAGACAGCTGTCCAGAGGAACCCCAACTACGAAT GAAAAATAATGAAGAAGCGGAAGACTATGATGATGA	2084
	TCATCATCATAGTCTTCCGCTTCTTCATTATTTTTCATTCTAG TTGGGGTTCCTCTGGACAGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAACAATGTC	2085
	AGACAGCTGTCCAGAGG	2086
	CCTCTGGACAGCTGTCT	2087
Haemophilia A Arg336Term aCGA-TGA	ACTCCAGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCG GAAGACTATGATGATGATCTTACTGATTCTGAAATGG	2088

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCATTTGAGAATCAGTAAGATCATCATAGTCTTCCGCTTC TTCATTATTTTTCATTGCTAGTTGGGGTTCTCTGGACAGCTG TCTACTTTGACATAAGCTTCCATGCCATCTGGAGT	2089
	CCCAACTAGGAATGAAA	2090
	TTTCATTGCTAGTTGGG	2091
Haemophilia A Arg372Cys tCGC-TGC	GATTCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTC CTTCCTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGG	2092
	CCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGATG CTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGGAGAGTT GTCATCATCAAACCTGACCACATCCATTTGAGAATC	2093
	TCCAAATTGCTCAGTT	2094
	AACTGAGCGAATTTGGA	2095
Haemophilia A Arg372His CGC-CAC	ATTCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCC TTCTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAAA ACTTGGGTACATTACATTGCTGCTGAAGAGGAGGA	2096
	TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGGAGAGT TGTCATCATCAAACCTGACCACATCCATTTGAGAAT	2097
	CCAAATTGCTCAGTTG	2098
	CAACTGAGCGAATTTGG	2099
Haemophilia A Ser373Leu TCA-TTA	CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAAA TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG	2100
	CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTGAG	2101
	AATTCGCTCAGTTGCCA	2102
	TGGCAACTGAGCGAATT	2103
Haemophilia A Ser373Pro cTCA-CCA	TCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTT CCTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAAA TTGGGTACATTACATTGCTGCTGAAGAGGAGGACT	2104
	AGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGG ATGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGGAGA GTTGTCATCATCAAACCTGACCACATCCATTTGAGA	2105
	AAATTCGCTCAGTTGCC	2106
	GGCAACTGAGCGAATT	2107
Haemophilia A Ser373Term TCA-TAA	CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAAA TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG	2108

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG	2109
	AATTCGCTCAGTTGCCA	2110
	TGGCAACTGAGCGAATT	2111
Haemophilia A Ile386Phe cATT-TTT	CCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTA AAACTTGGGTACATTACATTGCTGCTGAAGAGGAGGACTGGG ACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGT	2112
	ACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCAG TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGG	2113
	TACATTACATTGCTGCT	2114
	AGCAGCAATGTAATGTA	2115
Haemophilia A Ile386Ser ATT-AGT	CTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGGACTGGGA CTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGTA	2116
	TACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCA GTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGA TGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAG	2117
	ACATTACATTGCTGCTG	2118
	CAGCAGCAATGTAATGT	2119
Haemophilia A Glu390Gly GAG-GGG	AAATTCGCTCAGTTGCCAAGAAGCATCCTAAACTTGGGTACA TTACATTGCTGCTGAAGAGGAGGACTGGGACTATGCTCCCTT AGTCCTCGCCCCCGATGACAGGTAAGCACTTTTTGA	2120
	TCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGACTAAGGGA GCATAGTCCCAGTCCTCCTCTTCAGCAGCAATGTAATGTACC CAAGTTTTAGGATGCTTCTTGGCAACTGAGCGAATTT	2121
	TGCTGAAGAGGAGGACT	2122
	AGTCCTCCTCTTCAGCA	2123
Haemophilia A Trp393Gly cTGG-GGG	TCAGTTGCCAAGAAGCATCCTAAACTTGGGTACATTACATTG CTGCTGAAGAGGAGGACTGGGACTATGCTCCCTTAGTCCTCG CCCCCGATGACAGGTAAGCACTTTTTGACTATTGGT	2124
	ACCAATAGTCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGA CTAAGGGAGCATAGTCCCAGTCCTCCTCTTCAGCAGCAATGT AATGTACCCAAGTTTTAGGATGCTTCTTGGCAACTGA	2125
	AGGAGGACTGGGACTAT	2126
	ATAGTCCCAGTCCTCCT	2127
Haemophilia A Lys408Ile AAA-ATA	GCCTACCTAGAATTTTTCTTCCCAACCTCTCATCTTTTTTCTC TTATACAGAAGTTATAAAAGTCAATATTTGAACAATGGCCCTC AGCGGATTGGTAGGAAGTACAAAAAGTCCGATT	2128

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AATCGGACTTTTTGTACTTCCTACCAATCCGCTGAGGGCCAT TGTTCAAATATTGACTTTTATAACTTCTGTATAAGAGAAAAAA GATGAGAGGTTGGGAAGAAAATTCTAGGTAGGC	2129
	AAGTTATAAAAGTCAAT	2130
	ATTGACTTTTATAACTT	2131
Haemophilia A Leu412Phe TTGa-TTT	TTTTCTTCCCAACCTCTCATCTTTTTTCTCTTATACAGAAGTT ATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAG GAAGTACAAAAAGTCCGATTTATGGCATAACACA	2132
	TGTGTATGCCATAAATCGGACTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATAACTTCTGT ATAAGAGAAAAAAGATGAGAGGTTGGGAAGAAAA	2133
	CAATATTTGAACAATGG	2134
	CCATTGTTCAAATATTG	2135
Haemophilia A Arg418Trp gCGG-TGG	TCATCTTTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTG AACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTC CGATTTATGGCATAACACAGATGAAACCTTTAAGA	2136
	TCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTTG TACTTCCTACCAATCCGCTGAGGGCCATTGTTCAAATATTGAC TTTTATAACTTCTGTATAAGAGAAAAAAGATGA	2137
	GCCCTCAGCGGATTGGT	2138
	ACCAATCCGCTGAGGGC	2139
Haemophilia A Gly420Val GGT-GTT	TTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTGAACAAT GGCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTCCGATTT ATGGCATAACAGATGAAACCTTTAAGACTCGTGA	2140
	TCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGA CTTTTTTGTACTTCCTACCAATCCGCTGAGGGCCATTGTTCAA ATATTGACTTTTATAACTTCTGTATAAGAGAAAAA	2141
	GCGGATTGGTAGGAAGT	2142
	ACTTCCTACCAATCCGC	2143
Haemophilia A Lys425Arg AAA-AGA	GAAGTTATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGAT TGGTAGGAAGTACAAAAAGTCCGATTTATGGCATAACACAGAT GAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA	2144
	TCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT ATGCCATAAATCGGACTTTTTGTACTTCCTACCAATCCGCTG AGGGCCATTGTTCAAATATTGACTTTTATAACTTC	2145
	GTACAAAAAGTCCGAT	2146
	ATCGGACTTTTTGTAC	2147
Haemophilia A Arg427Term cCGA-TGA	TATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTA GGAAGTACAAAAAGTCCGATTTATGGCATAACACAGATGAAAC CTTTAAGACTCGTGAAGCTATTCAGCATGAATCAG	2148

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGATTCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATC TGTGTATGCCATAAATCGGACTTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATA	2149
	AAAAAGTCCGATTTATG	2150
	CATAAATCGGACTTTTT	2151
Haemophilia A Tyr431Asn aTAC-AAC	TATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAA AAAGTCCGATTTATGGCATAACACAGATGAAACCTTTAAGACTC GTGAAGCTATTCAGCATGAATCAGGAATCTTGGGAC	2152
	GTCCCAAGATTCCTGATTCATGCTGAATAGCTTCACGAGTCTT AAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTTGTAC TTCTACCAATCCGCTGAGGGCCATTGTTCAAATA	2153
	TTATGGCATAACACAGAT	2154
	ATCTGTGTATGCCATAA	2155
Haemophilia A Thr435Ile ACC-ATC	GCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTCCGATTTA TGGCATAACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCA GCATGAATCAGGAATCTTGGGACCTTTACTTTATGG	2156
	CCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAG CTTCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCG GACTTTTTTGTACTTCCTACCAATCCGCTGAGGGC	2157
	AGATGAAACCTTTAAGA	2158
	TCTTAAAGGTTTCATCT	2159
Haemophilia A Pro451Leu CCT-CTT	ACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA ATCAGGAATCTTGGGACCTTTACTTTATGGGGAAGTTGGAGA CACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGTC	2160
	GACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAA CTTCCCCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTG AATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT	2161
	CTTGGGACCTTTACTTT	2162
	AAAGTAAAGGTCCCAAG	2163
Haemophilia A Pro451Thr aCCT-ACT	TACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATG AATCAGGAATCTTGGGACCTTTACTTTATGGGGAAGTTGGAGA CACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGT	2164
	ACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAACT TCCCCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAA TAGCTTCACGAGTCTTAAAGGTTTCATCTGTGTA	2165
	TCTTGGGACCTTTACTT	2166
	AAGTAAAGGTCCCAAGA	2167
Haemophilia A Gly455Arg tGGG-AGG	ACCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCT TGGGACCTTTACTTTATGGGGAAGTTGGAGACACACTGTTGG TAAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGA	2168

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAGT GTGTCTCCAACCTCCCAATAAAGTAAAGGTCCCAAGATTCTG ATTCATGCTGAATAGCTTCACGAGTCTTAAAGGT	2169
	TACTTTATGGGGAAGTT	2170
	AACTTCCCAATAAAGTA	2171
Haemophilia A Gly455Glu GGG-GAG	CCTTTAAGACTCGTGAAGCTATTGAGCATGAATCAGGAATCTT GGGACCTTTACTTTATGGGGAAGTTGGAGACACACTGTTGGT AAGTTGAAGAAAAGATTAAAGGTCAGGTAAGAAGAA	2172
	TTCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAG TGTGTCTCCAACCTCCCAATAAAGTAAAGGTCCCAAGATTCTT GATTCATGCTGAATAGCTTCACGAGTCTTAAAGG	2173
	ACTTTATGGGGAAGTTG	2174
	CAACTTCCCAATAAAGT	2175
Haemophilia A Asp459Asn aGAC-AAC	CGTGAAGCTATTGAGCATGAATCAGGAATCTTGGGACCTTTAC TTTATGGGGAAGTTGGAGACACACTGTTGGTAAGTTGAAGAA AAGATTAAAGGTCAGGTAAGAAGAAAAAGTCTGGAG	2176
	CTCCAGACTTTTTCTTCTTACCTGACCTTAAATCTTTCTTCAA CTTACCAACAGTGTGTCTCCAACCTCCCAATAAAGTAAAGGTC CCAAGATTCTGATTCATGCTGAATAGCTTCACG	2177
	AAGTTGGAGACACACTG	2178
	CAGTGTGTCTCCAACCT	2179
Haemophilia A Phe465Cys TTT-TGT	TGTTGATCCTAGTCGTTTTAGGATTTGATCTTAGATCTCGCTTA TACTTTCAGATTATATTAAAGAATCAAGCAAGCAGACCATATAA CATCTACCCTCACGGAATCACTGATGTCCGTCC	2180
	GGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGT CTGCTTGCTTGATTCTTAAATATAATCTGAAAGTATAAGCGAG ATCTAAGATCAAATCCTAAAACGACTAGGATCAACA	2181
	GATTATATTAAAGAATC	2182
	GATTCTTAAATATAATC	2183
Haemophilia A Ala469Gly GCA-GGA	TCGTTTTAGGATTTGATCTTAGATCTCGCTTATACTTTCAGATT ATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTC ACGGAATCACTGATGTCCGTCTTTGTATTCAAG	2184
	CTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAG ATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAA GTATAAGCGAGATCTAAGATCAAATCCTAAAACGA	2185
	GAATCAAGCAAGCAGAC	2186
	GTCTGCTTGCTTGATTG	2187
Haemophilia A Arg471Gly cAGA-GGA	TTAGGATTTGATCTTAGATCTCGCTTATACTTTCAGATTATATT TAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGG AATCACTGATGTCCGTCTTTGTATTCAAGGAGAT	2188

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAG GGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATC TGAAAGTATAAGCGAGATCTAAGATCAAATCCTAA	2189
	AAGCAAGCAGACCATAT	2190
	ATATGGTCTGCTTGCTT	2191
Haemophilia A Tyr473Cys TAT-TGT	TTGATCTTAGATCTCGCTTATACTTTCAGATTATATTTAAGAAT CAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACT GATGTCCGTCCTTTGTATTCAAGGAGATTACCAA	2192
	TTTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCC CGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAA TATAATCTGAAAGTATAAGCGAGATCTAAGATCAA	2193
	CAGACCATATAACATCT	2194
	AGATGTTATATGGTCTG	2195
Haemophilia A Tyr473His aTAT-CAT	TTTGATCTTAGATCTCGCTTATACTTTCAGATTATATTTAAGAA TCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACT GATGTCCGTCCTTTGTATTCAAGGAGATTACCAA	2196
	TTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCC GTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAAT ATAATCTGAAAGTATAAGCGAGATCTAAGATCAA	2197
	GCAGACCATATAACATC	2198
	GATGTTATATGGTCTGC	2199
Haemophilia A Ile475Thr ATC-ACC	TTAGATCTCGCTTATACTTTCAGATTATATTTAAGAATCAAGCA AGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCC GTCCTTTGTATTCAAGGAGATTACCAAAGGTAA	2200
	TTACCTTTTGGTAATCTCCTTGAATACAAAGGACGGACATCAG TGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATT CTTAAATATAATCTGAAAGTATAAGCGAGATCTAA	2201
	ATATAACATCTACCCTC	2202
	GAGGGTAGATGTTATAT	2203
Haemophilia A Gly479Arg cGGA-AGA	TTATACTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATA TAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT TCAAGGAGATTACCAAAGGTAAATATTCCCTCG	2204
	CGAGGGAATATTTACCTTTTGGTAATCTCCTTGAATACAAAGG ACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCT GCTTGCTTGATTCTTAAATATAATCTGAAAGTATAA	2205
	ACCCTCACGGAATCACT	2206
	AGTGATTCCGTGAGGGT	2207
Haemophilia A Thr522Ser aACT-TCT	CCAATTCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGA CTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGA CCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAG	2208

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CTCTCTCCATATTAACGAACTAGAGTAATAGCGGGTCAGGC ACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT CCATTTATATTTGAATATTTCTCCTGGCAGAATTGG	2209
	ATGGGCCCACTAAATCA	2210
	TGATTTAGTTGGCCCAT	2211
Haemophilia A Asp525Asn aGAT-AAT	CCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG ATGGGCCCACTAAATCAGATCCTCGGTGCCTGACCCGCTATT ACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTT	2212
	AAGCTAGATCTCTCTCCATATTAACGAACTAGAGTAATAGCG GGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTAC AGTCACTGTCCATTTATATTTGAATATTTCTCCTGG	2213
	CTAAATCAGATCCTCGG	2214
	CCGAGGATCTGATTTAG	2215
Haemophilia A Arg527Trp tCGG-TGG	GAAATATTCAAATATAAATGGACAGTGACTGTAGAAGATGGGC CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGAC	2216
	GTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAGTA ATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATC TTCTACAGTCACTGTCCATTTATATTTGAATATTTCT	2217
	CAGATCCTCGGTGCCTG	2218
	CAGGCACCGAGGATCTG	2219
Haemophilia A Arg531Cys cCGC-TGC	TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCA GATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATA TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC	2220
	GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAA CGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATT TAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATA	2221
	GCCTGACCCGCTATTAC	2222
	GTAATAGCGGGTCAGGC	2223
Haemophilia A Arg531Gly cCGC-GGC	TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCA GATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATA TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC	2224
	GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAA CGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATT TAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATA	2225
	GCCTGACCCGCTATTAC	2226
	GTAATAGCGGGTCAGGC	2227
Haemophilia A Arg531His CGC-CAC	ATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAG ATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATAT GGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCT	2228

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
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	CCTGACCCGCTATTACT	2230
	AGTAATAGCGGGTCAGG	2231
Haemophilia A Ser534Pro cTCT-CCT	ACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGG TGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAG ATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCT	2232
	AGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCT CCATATTAAACGAACTAGAGTAATAGCGGGTCAGGCACCGAG GATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT	2233
	GCTATTACTCTAGTTTC	2234
	GAACTAGAGTAATAGC	2235
Haemophilia A Ser535Gly tAGT-GGT	GTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGC CTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATC TAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCT	2236
	AGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTC TCTCCATATTAAACGAACTAGAGTAATAGCGGGTCAGGCACC GAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCAC	2237
	ATTACTCTAGTTTCGTT	2238
	AACGAACTAGAGTAAT	2239
Haemophilia A Val537Asp GTT-GAT	TAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCC GCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTC AGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGA	2240
	TCTTTGTAGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCT AGATCTCTCTCCATATTAAACGAACTAGAGTAATAGCGGGTCA GGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTA	2241
	TAGTTTCGTTAATATGG	2242
	CCATATTAAACGAACTA	2243
Haemophilia A Arg541Thr AGA-ACA	CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGG CCCTCTCCTCATCTGCTACAAAGAATCTGTAGATCA	2244
	TGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAATG AGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGT AATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTG	2245
	TATGGAGAGAGATCTAG	2246
	CTAGATCTCTCTCCATA	2247
Haemophilia A Asp542Gly GAT-GGT	CTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTT CGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCC TCTCCTCATCTGCTACAAAGAATCTGTAGATCAAAG	2248

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCA ATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAG AGTAATAGCGGGTCAGGCACCGAGGATCTGATTAG	2249
	GGAGAGAGATCTAGCTT	2250
	AAGCTAGATCTCTCTCC	2251
Haemophilia A Asp542His aGAT-CAT	ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAA	2252
	TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAAT GAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAG TAATAGCGGGTCAGGCACCGAGGATCTGATTAGT	2253
	TGGAGAGAGATCTAGCT	2254
	AGCTAGATCTCTCTCCA	2255
Haemophilia A Asp542Tyr aGAT-TAT	ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAA	2256
	TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAAT GAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAG TAATAGCGGGTCAGGCACCGAGGATCTGATTAGT	2257
	TGGAGAGAGATCTAGCT	2258
	AGCTAGATCTCTCTCCA	2259
Haemophilia A Glu557Term aGAA-TAA	GTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCT CTCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACC AGGTGAGTTCTTGCCTTTCCAAGTGCTGGGTTTCAT	2260
	ATGAAACCCAGCACTTGGAAAGGCAAGAACTCACCTGGTTTC CTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGC CAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAC	2261
	GCTACAAAGAATCTGTA	2262
	TACAGATTCTTTGTAGC	2263
Haemophilia A Ser558Phe TCT-TTT	ATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCC TCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGGT GAGTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTC	2264
	GAGAATGAAACCCAGCACTTGGAAAGGCAAGAACTCACCTGG TTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAG GGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATAT	2265
	CAAAGAATCTGTAGATC	2266
	GATCTACAGATTCTTTG	2267
Haemophilia A Val559Ala GTA-GCA	TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCA TCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGGTGA GTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTCAGT	2268

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGAGAATGAAACCCAGCACTTGGAAAGGCAAGAACTCACC TGGTTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGA GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCA	2269
	AGAATCTGTAGATCAAA	2270
	TTTGATCTACAGATTCT	2271

EXAMPLE 14
Hemophilia - Factor IX Deficiency

The attached table discloses the correcting oligonucleotide base sequences for the Factor IX oligonucleotides of the invention.

Table 21
Factor IX Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia B Asn2Asp tAAT-GAT	ATTTGAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTGAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2272
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT GTTGGCGTTTTTCATGATCAAGAAAACTGAAAT	2273
	AGAGGTATAATTGAGGT	2274
	ACCTGAATTATACCTCT	2275
Haemophilia B Asn2Ile AAT-ATT	TTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAAT CGGCCAAAGAGGTATAATTGAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2276
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTC TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT TGTTGGCGTTTTTCATGATCAAGAAAACTGAAA	2277
	GAGGTATAATTGAGGT	2278
	TACCTGAATTATACCTC	2279
Haemophilia B Asn2Tyr tAAT-TAT	ATTTGAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTGAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2280
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT GTTGGCGTTTTTCATGATCAAGAAAACTGAAAT	2281

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AGAGGTATAATTCAGGT	2282
	ACCTGAATTATACCTCT	2283
Haemophilia B Ser3Pro TCA-CCA	TCAGTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATC GGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCA AGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT	2284
	ACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAAC TCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTGAGAA TTTTGTTGGCGTTTTTCATGATCAAGAAAACTGA	2285
	GGTATAATTCAGGTAAA	2286
	TTTACCTGAATTATACC	2287
Haemophilia B Gly4Asp GGT-GAT	TTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCC AAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGG AACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAG	2288
	CTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC AAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCA GAATTTTGTTGGCGTTTTTCATGATCAAGAAAAA	2289
	TAATTCAGGTAAATTGG	2290
	CCAATTTACCTGAATTA	2291
Haemophilia B Gly4Ser aGGT-AGT	GTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGC CAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAT	2292
	TACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACA AACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCA GAATTTTGTTGGCGTTTTTCATGATCAAGAAAAAC	2293
	ATAATTCAGGTAAATTG	2294
	CAATTTACCTGAATTAT	2295
Haemophilia B Lys5Glu TAAA-GAA	TTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAA AGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAA CCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT	2296
	AACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGA ACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATT CAGAATTTTGTTGGCGTTTTTCATGATCAAGAAA	2297
	ATTCAGGTAAATTGGAA	2298
	TTCCAATTTACCTGAAT	2299
Haemophilia B Glu7Ala GAA-GCA	ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTA TAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAAACCTTGAG AGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA	2300
	TCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTT CCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTG GCCGATTGAGAATTTTGTTGGCGTTTTTCATGAT	2301

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAAATTGGAAGAGTTTG	2302
	CAAAC <u>T</u> CTTCCAATTTA	2303
Haemophilia B Glu7Lys gGAA-AAA	GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGG TATAATTCAGGTAAATTGGAAGAGTTTGTTCAGGGGAACCTTG AGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAG	2304
	CTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTT CCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGG CCGATTCAGAATTTTGTGGCGTTTTCATGATC	2305
	GTAAATTGGAAGAGTTT	2306
	AAACTCTTCCAATTTAC	2307
Haemophilia B Glu7Val GAA-GTA	ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTA TAATTCAGGTAAATTGGAAGAGTTTGTTCAGGGGAACCTTGAG AGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA	2308
	TCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTT CCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTG GCCGATTCAGAATTTTGTGGCGTTTTCATGAT	2309
	TAAATTGGAAGAGTTTG	2310
	CAAAC <u>T</u> CTTCCAATTTA	2311
Haemophilia B Glu8Ala GAG-GCG	ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA TTCAGGTAAATTGGAAGAGTTTGTTCAGGGGAACCTTGAGAG AGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC	2312
	GCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCT TTGGCCGATTCAGAATTTTGTGGCGTTTTCAT	2313
	ATTGGAAGAGTTTGTTT	2314
	GAACAACTCTTCCAAT	2315
Haemophilia B Glu8Gly GAG-GGG	ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA TTCAGGTAAATTGGAAGAGTTTGTTCAGGGGAACCTTGAGAG AGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC	2316
	GCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCT TTGGCCGATTCAGAATTTTGTGGCGTTTTCAT	2317
	ATTGGAAGAGTTTGTTT	2318
	GAACAACTCTTCCAAT	2319
Haemophilia B Phe9Cys TTT-TGT	AAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTC AGGTAAATTGGAAGAGTTTGTTCAGGGGAACCTTGAGAGAGA ATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACG	2320
	CGTGCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTC AAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATAC CTCTTTGGCCGATTCAGAATTTTGTGGCGTTTT	2321

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGAAGAGT <u>T</u> TGTTCAAG	2322
	CTTGAACAA <u>A</u> CTCTTCC	2323
Haemophilia B Phe9Ile gTTT-ATT	GAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATT CAGGTAAATTGGAAGAGT <u>T</u> TGTTCAAGGGAACCTTGAGAGAG AATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC	2324
	GTGCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCA AGGTTCCCTTGAACAA <u>A</u> CTCTTCCAATTTACCTGAATTATACC TCTTTGGCCGATTGAGAATTTTGTGCGGTTTTTC	2325
	TGGAAGAGT <u>T</u> TGTTCAA	2326
	TTGAACAA <u>A</u> CTCTTCCA	2327
Haemophilia B Arg(-1)Ser AGGt-AGC	TTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTC TGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTT TGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA	2328
	TTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCC AATTTACCTGAATTATAC <u>C</u> CTCTTTGGCCGATTGAGAATTTTGT GGCGTTTTTCATGATCAAGAAAACTGAAATGTAA	2329
	CCAAAGAG <u>G</u> TATAATTC	2330
	GAATTATAC <u>C</u> CTCTTTGG	2331
Haemophilia B Arg(-1)Thr AGG-ACG	TTTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATT CTGAATCGGCCAAAGAG <u>G</u> TATAATTCAGGTAAATTGGAAGAG TTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGA	2332
	TCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCA ATTTACCTGAATTATAC <u>C</u> CTCTTTGGCCGATTGAGAATTTTGTG GCGTTTTTCATGATCAAGAAAACTGAAATGTAA	2333
	GCCAAAGAG <u>G</u> TATAATT	2334
	AATTATAC <u>C</u> CTCTTTGGC	2335
Haemophilia B Lys(-2)Asn AAGa-AAT	CTTTTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAA TTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGA GTTTGTTCAAGGGAACCTTGAGAGAGAATGTATG	2336
	CATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAAT TTACCTGAATTATACCT <u>C</u> TTTGGCCGATTGAGAATTTTGTG CGTTTTTCATGATCAAGAAAACTGAAATGTAAAAG	2337
	CGGCCAAAG <u>A</u> GAGGTATAA	2338
	TTATACCT <u>C</u> TTTGGCCG	2339
Haemophilia B Arg(-4)Gln CGG-CAG	AATTATTCTTTTACATTTCAGTTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATC <u>G</u> GCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGA	2340
	TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGC <u>C</u> GATTGAGAATTTTGTGCGTTTTCA TGATCAAGAAAACTGAAATGTAAAAGAATAATT	2341

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGAATCGGCCAAAGA	2342
	TCTTTGGCCGATTCAGA	2343
Haemophilia B Arg(-4)Leu CGG-CTG	AATTATTCTTTACATTTAGTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGA	2344
	TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCA TGATCAAGAAAACTGAAATGTAAAAGAATAATT	2345
	TCTGAATCGGCCAAAGA	2346
	TCTTTGGCCGATTCAGA	2347
Haemophilia B Arg(-4)Trp tCGG-TGG	GAATTATTCTTTACATTTAGTTTTCTTGATCATGAAAACGC CAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAA TTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAG	2348
	CTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGA ATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCAT GATCAAGAAAACTGAAATGTAAAAGAATAATTC	2349
	TTCTGAATCGGCCAAAG	2350
	CTTTGGCCGATTCAGAA	2351
Haemophilia B Gln11Term tCAA-TAA	GCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTA AATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTAT GGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAG	2352
	CTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACATTCT CTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAAT TATACCTCTTTGGCCGATTCAGAATTTTGTTGGC	2353
	AGTTTGTTCAAGGGAAC	2354
	GTTCCCTTGAACAACT	2355
Haemophilia B Gly12Ala GGG-GCG	ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT GGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTT	2356
	AAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTCAGAATTTTGTT	2357
	TGTTCAAGGGAACCTTG	2358
	CAAGGTTCCCTTGAACA	2359
Haemophilia B Gly12Arg aGGG-AGG	AACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGG AAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTT	2360
	AAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACAT TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGCCGATTCAGAATTTTGTT	2361

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTGTTCAAGGGAACCTT	2362
	AAGGTTCCCTTGAACAA	2363
Haemophilia B Gly12Glu GGG-GAG	ACAAAATTCTGAATCGGCCAAAGAGGTATAATT CAGGTAAATT GGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTT	2364
	AAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTCAGAATTTTGT	2365
	TGTTCAAGGGAACCTTG	2366
	CAAGGTTCCCTTGAACA	2367
Haemophilia B Glu17Gln aGAA-CAA	CGGCCAAAGAGGTATAATT CAGGTAAATTGGAAGAGTTTGTT C AAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT TTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAA	2368
	TTTCAGTGTTTTCAAAACTTCTCGTGCTTCTTCAAACTACAC TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCG	2369
	TTGAGAGAGAATGTATG	2370
	CATACATTCTCTCTCAA	2371
Haemophilia B Glu17Lys aGAA-AAA	CGGCCAAAGAGGTATAATT CAGGTAAATTGGAAGAGTTTGTT C AAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT TTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAA	2372
	TTTCAGTGTTTTCAAAACTTCTCGTGCTTCTTCAAACTACAC TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCG	2373
	TTGAGAGAGAATGTATG	2374
	CATACATTCTCTCTCAA	2375
Haemophilia B Cys18Arg aTGT-CGT	CCAAAGAGGTATAATT CAGGTAAATTGGAAGAGTTTGTTCAAG GGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTG AAGAAGCACGAGAAGTTTTTGAACAACTGAAAGAA	2376
	TTCTTT CAGTGTTTTCAAAACTTCTCGTGCTTCTTCAAACTA CACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA ACTCTTCCAATTTACCTGAATTATACCTCTTTGG	2377
	AGAGAGAATGTATGGAA	2378
	TTCCATACATTCTCTCT	2379
Haemophilia B Cys18Tyr TGT-TAT	CAAAGAGGTATAATT CAGGTAAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAA GAAGCACGAGAAGTTTTTGAACAACTGAAAGAAC	2380
	GTTCTTT CAGTGTTTTCAAAACTTCTCGTGCTTCTTCAAACT ACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA ACTCTTCCAATTTACCTGAATTATACCTCTTTG	2381

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGAGAAT <u>G</u> TATGGAAG	2382
	CTCCATAC <u>A</u> TTCTCTC	2383
Haemophilia B Glu20Val GAA-GTA	GGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAG	2384
	CTCACTGTTCTTTCACTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACC	2385
	ATGTATGGAAGAAAAGT	2386
	ACTTTTCTTCCATACAT	2387
Haemophilia B Glu21Lys aGAA-AAA	TATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTA	2388
	TACTCACTGTTCTTTCACTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATA	2389
	GTATGGAAGAAAAGTGT	2390
	ACACTTTTCTTCCATAC	2391
Haemophilia B Cys23Arg gTGT-CGT	TCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAA GTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCA	2392
	TGGAAATACTCACTGTTCTTTCACTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGA	2393
	AAGAAAAGTGTAGTTTT	2394
	AAAACACTACTTTTCTT	2395
Haemophilia B Cys23Tyr TGT-TAT	CAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAG AATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGT TTTTGAAAACACTGAAAGAACAGTGAGTATTTCCAC	2396
	GTGGAAATACTCACTGTTCTTTCACTGTTTTCAAAAACCTTCTC GTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCA AGGTTCCCTTGAACAACTCTTCCAATTTACCTG	2397
	AGAAAAGTGTAGTTTTG	2398
	CAAACTACACTTTTCT	2399
Haemophilia B Phe25Ser TTT-TCT	AATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTAT GGAAGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTTTTGAA AACACTGAAAGAACAGTGAGTATTTCCACATAATA	2400
	TATTATGTGGAAATACTCACTGTTCTTTCACTGTTTTCAAAAAC TTCTCGTGCTTCTTCAAAAACACTACTTTTCTTCCATACATTCTC TCTCAAGGTTCCCTTGAACAACTCTTCCAATT	2401

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTGTAGTTTGAAGAAG	2402
	CTTCTTCAA <u>A</u> ACTACAC	2403
Haemophilia B Glu26Gln tGAA-CAA	TTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATG GAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGA AACTGAAAGAACAGTGAGTATTTCCACATAATACC	2404
	GGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAA ACTTCTCGTGCTTCTTCAA <u>A</u> ACTACACTTTTCTTCCATACATT TCTCTCAAGGTTCCCTTGAACAAACTCTTCCAA	2405
	GTAGTTTTGAAGAAGCA	2406
	TGCTTCTTCAA <u>A</u> ACTAC	2407
Haemophilia B Glu27Ala GAA-GCA	AAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC	2408
	GAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTT CAAAA <u>A</u> CTTCTCGTGCTTCTTCAA <u>A</u> ACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT	2409
	TTTTGAAGAAGCACGAG	2410
	CTCGTGCTTCTTCAAAA	2411
Haemophilia B Glu27Asp GAAG-GAC	AGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGAAGA AAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACACT GAAAGAACAGTGAGTATTTCCACATAATACCCTTCA	2412
	TGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTT TCAAAA <u>A</u> CTTCTCGTGCTTCTTCAA <u>A</u> ACTACACTTTTCTTCCAT ACATTCTCTCTCAAGGTTCCCTTGAACAAACTCT	2413
	TTTGAAGAAGCACGAGA	2414
	TCTCGTGCTTCTTCAA	2415
Haemophilia B Glu27Lys aGAA-AAA	GAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGAA GAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACACA CTGAAAGAACAGTGAGTATTTCCACATAATACCCTT	2416
	AAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTT AAAACTTCTCGTGCTTCTTCAA <u>A</u> ACTACACTTTTCTTCCATAC ATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT	2417
	GTTTTGAAGAAGCACGA	2418
	TCGTGCTTCTTCAAAC	2419
Haemophilia B Glu27Val GAA-GTA	AAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC	2420
	GAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTT CAAAA <u>A</u> CTTCTCGTGCTTCTTCAA <u>A</u> ACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT	2421

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTTGAAGAAGCACGAG	2422
	CTCGTGCTTCTTCAAAA	2423
Haemophilia B Arg29Gln CGA-CAA	TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATGC	2424
	GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCAG TGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTTCT TCCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2425
	AGAAGCACGAGAAGTTT	2426
	AAACTTCTCGTGCTTCT	2427
Haemophilia B Arg29Pro CGA-CCA	TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATGC	2428
	GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCAG TGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTTCT TCCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2429
	AGAAGCACGAGAAGTTT	2430
	AAACTTCTCGTGCTTCT	2431
Haemophilia B Arg29Term aCGA-TGA	TTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATG	2432
	CATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCAGT GTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTTCTT CCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2433
	AAGAAGCACGAGAAGTT	2434
	AACTTCTCGTGCTTCTT	2435
Haemophilia B Glu30Lys aGAA-AAA	GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGT AGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAA CAGTGAGTATTTCCACATAATACCCTTCAGATGCAG	2436
	CTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTC AGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTT CTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC	2437
	AAGCACGAGAAGTTTTT	2438
	AAAACTTCTCGTGCTT	2439
Haemophilia B Glu30Term aGAA-TAA	GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGT AGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAA CAGTGAGTATTTCCACATAATACCCTTCAGATGCAG	2440
	CTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTC AGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTT CTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC	2441

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AAGCACGAGAAGTTTT	2442
	AAAACTTCTCGTGCTT	2443
Haemophilia B Glu33Asp GAAa-GAC	CCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAA GCACGAGAAGTTTTGAAACACTGAAAGAACAGTGAGTATTT CCACATAATACCCTTCAGATGCAGAGCATAGAATA	2444
	TATTCTATGCTCTGCATCTGAAGGGTATTATGTGGAAATACTC ACTGTTCTTTCAGTGTTTCAAAAACCTTCTCGTGCTTCTTCAA ACTACACTTTTCTTCCATACATTCTCTCTCAAGG	2445
	GTTTTGAAACACTGA	2446
	TCAGTGTTTCAAAAAC	2447
Haemophilia B Glu33Term tGAA-TAA	AACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAG AAGCACGAGAAGTTTTGAAACACTGAAAGAACAGTGAGTAT TTCCACATAATACCCTTCAGATGCAGAGCATAGAA	2448
	TTCTATGCTCTGCATCTGAAGGGTATTATGTGGAAATACTCAC TGTTCTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAC TACACTTTTCTTCCATACATTCTCTCTCAAGGTT	2449
	AAGTTTTGAAACACT	2450
	AGTGTTTTCAAAAACCTT	2451
Haemophilia B Trp42Term TGG-TAG	CAAAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTT TATAGACTGAATTTTGGAAGCAGTATGTTGGTAAGCAATTCAT TTTATCCTCTAGCTAATATATGAAACATATGAG	2452
	CTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGCTT ACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAATAAAAG AAGACAAATTAACGGTAATATCTAAAGTGTTTTG	2453
	TGAATTTTGGAAGCAGT	2454
	ACTGCTTCCAAAATTCA	2455
Haemophilia B Lys43Glu gAAG-GAG	AAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTA TAGACTGAATTTTGGAAGCAGTATGTTGGTAAGCAATTCATTT TATCCTCTAGCTAATATATGAAACATATGAGAA	2456
	TTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGC TTACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAATAAAA GAAGACAAATTAACGGTAATATCTAAAGTGTTT	2457
	AATTTTGGAAGCAGTAT	2458
	ATACTGCTTCCAAAATT	2459
Haemophilia B Gln44Term gCAG-TAG	CACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTATAG ACTGAATTTTGGAAGCAGTATGTTGGTAAGCAATTCATTTTATC CTCTAGCTAATATATGAAACATATGAGAATTA	2460
	TAATTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAAT TGCTTACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAATA AAAGAAGACAAATTAACGGTAATATCTAAAGTG	2461

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTGGAAGCAGTATGTT	2462
	AACATACTGCTTCCAAA	2463
Haemophilia B Asp49Gly GAT-GGT	CCGGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAATGGCGGCAGTTGCAAGGATGACATTAATTCCTA	2464
	TAGGAATTAATGTCATCCTTGCAACTGCCGCCATTAAACATG GATTGGACTCACACTGATCTCCATCTTTGAGATAGGTAAAGAAATTGAATTGGCACGTAACTGCTTAGAATGCCCGG	2465
	AGATGGAGATCAGTGTG	2466
	CACACTGATCTCCATCT	2467
Haemophilia B Gln50His CAGt-CAC	GCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAA	2468
	TTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTAAA CATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTAAAGAAATTGAATTGGCACGTAACTGCTTAGAATGC	2469
	GGAGATCAGTGTGAGTC	2470
	GACTCACACTGATCTCC	2471
Haemophilia B Gln50Pro CAG-CCG	GGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGA	2472
	TCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTAA GAAATTGAATTGGCACGTAACTGCTTAGAATGCC	2473
	TGGAGATCAGTGTGAGT	2474
	ACTCACACTGATCTCCA	2475
Haemophilia B Gln50Term tCAG-TAG	GGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATG	2476
	CATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTAAAGAAATTGAATTGGCACGTAACTGCTTAGAATGCC	2477
	ATGGAGATCAGTGTGAG	2478
	CTCACACTGATCTCCAT	2479
Haemophilia B Cys51Arg gTGT-CGT	CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAAT	2480
	ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTAAAGAAATTGAATTGGCACGTAACTGCTTAGAATG	2481

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GAGATCAGTGTGAGTCC	2482
	GGACTCACACTGATCTC	2483
Haemophilia B Cys51Ser gTGT-AGT	CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCT CAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAAT	2484
	ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTT AAGAAATTGAATTGGCACGTAAACTGCTTAGAATG	2485
	GAGATCAGTGTGAGTCC	2486
	GGACTCACACTGATCTC	2487
Haemophilia B Cys51Trp TGTg-TGG	TTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCA AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGT	2488
	ACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTT AAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGG TTAAGAAATTGAATTGGCACGTAAACTGCTTAGAA	2489
	GATCAGTGTGAGTCCAA	2490
	TTGGACTCACACTGATC	2491
Haemophilia B Glu52Term tGAG-TAG	TCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAA AGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGG CAGTTGCAAGGATGACATTAATTCCTATGAATGTT	2492
	AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAG GTTAAGAAATTGAATTGGCACGTAAACTGCTTAGA	2493
	ATCAGTGTGAGTCCAAT	2494
	ATTGGACTCACACTGAT	2495
Haemophilia B Pro55Ala tCCA-GCA	TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAG ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCT	2496
	AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACT GCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCT TTGAGATAGGTTAAGAAATTGAATTGGCACGTAAA	2497
	AGTCCAATCCATGTTTA	2498
	TAAACATGGATTGGACT	2499
Haemophilia B Pro55Arg CCA-CGA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2500
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2501

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTCCAATCCATGTTTAA	2502
	TTAAACATGGATTGGAC	2503
Haemophilia B Pro55Gln CCA-CAA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2504
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2505
	GTCCAATCCATGTTTAA	2506
	TTAAACATGGATTGGAC	2507
Haemophilia B Pro55Leu CCA-CTA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2508
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2509
	GTCCAATCCATGTTTAA	2510
	TTAAACATGGATTGGAC	2511
Haemophilia B Pro55Ser tCCA-TCA	TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAG ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCT	2512
	AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACT GCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCT TTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2513
	AGTCCAATCCATGTTTA	2514
	TAAACATGGATTGGACT	2515
Haemophilia B Cys56Arg aTGT-CGT	ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATC AGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGG ATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG	2516
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCA ACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT	2517
	CCAATCCATGTTTAAAT	2518
	ATTAAACATGGATTGG	2519
Haemophilia B Cys56Ser aTGT-AGT	ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATC AGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGG ATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG	2520
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCA ACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT	2521

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CCAATCCATGTTTAAAT	2522
	ATTTAAACATGGATTGG	2523
Haemophilia B Cys56Ser TGT-TCT	CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCA GTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGA TGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG	2524
	CCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG	2525
	CAATCCATGTTTAAATG	2526
	CATTTAAACATGGATTG	2527
Haemophilia B Cys56Tyr TGT-TAT	CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCA GTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGA TGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG	2528
	CCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG	2529
	CAATCCATGTTTAAATG	2530
	CATTTAAACATGGATTG	2531
Haemophilia B Asn58Lys AATg-AAG	ATTCATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAG TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTGAA	2532
	TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACT GATCTCCATCTTTGAGATAGGTTAAGAAATTGAAT	2533
	TGTTTAAATGGCGGCAG	2534
	CTGCCGCCATTTAAACA	2535
Haemophilia B Gly59Asp GGC-GAC	TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTC CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTGAAAGG	2536
	CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGT CATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA CTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA	2537
	TTTAAATGGCGGCAGTT	2538
	AACTGCCGCCATTTAAA	2539
Haemophilia B Gly59Val GGC-GTC	TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTC CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTGAAAGG	2540
	CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGT CATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA CTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA	2541

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTTAAATGGCGGCAGTT	2542
	AACTGCCGCCATTATAA	2543
Haemophilia B Gly59Ser tGGC-AGC	TTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGT CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAA TTCCTATGAATGTTGGTGTCCCTTTGGATTGAAG	2544
	CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTC ATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCACAC TGATCTCCATCTTTGAGATAGGTTAAGAAATTGAA	2545
	GTTTAAATGGCGGCAGT	2546
	ACTGCCGCCATTAAAC	2547
Haemophilia B Gly60Ser cGGC-AGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA ATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATTC CTATGAATGTTGGTGTCCCTTTGGATTGAAGGAA	2548
	TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT GTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCA CACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2549
	TAAATGGCGGCAGTTGC	2550
	GCAACTGCCGCCATTAA	2551
Haemophilia B Gly60Cys cGGC-TGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA ATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATTC CTATGAATGTTGGTGTCCCTTTGGATTGAAGGAA	2552
	TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT GTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCA CACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2553
	TAAATGGCGGCAGTTGC	2554
	GCAACTGCCGCCATTAA	2555
Haemophilia B Gly60Asp GGC-GAC	ATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA TCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATTC TATGAATGTTGGTGTCCCTTTGGATTGAAGGAAA	2556
	TTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAA TGTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTC ACACTGATCTCCATCTTTGAGATAGGTTAAGAAAT	2557
	AAATGGCGGCAGTTGCA	2558
	TGCAACTGCCGCCATT	2559
Haemophilia B Gly60Arg cGGC-CGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA ATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAATTC CTATGAATGTTGGTGTCCCTTTGGATTGAAGGAA	2560
	TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT GTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCA CACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2561

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAAATGGCGGCAGTTGC	2562
	GCAACTGCCGCCATTGA	2563
Haemophilia B Cys62Tyr TGC-TAC	TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATG TTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAA TGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG	2564
	CAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGG AATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATT GGACTCACACTGATCTCCATCTTTGAGATAGGTTA	2565
	CGGCAGTTGCAAGGATG	2566
	CATCCTTGCAACTGCCG	2567
Haemophilia B Cys62Ser TGC-TCC	TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATG TTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAA TGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG	2568
	CAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGG AATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATT GGACTCACACTGATCTCCATCTTTGAGATAGGTTA	2569
	CGGCAGTTGCAAGGATG	2570
	CATCCTTGCAACTGCCG	2571
Haemophilia B Cys62Term TGCα-TGA	AACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGT TTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAAT GTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGT	2572
	ACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGAT TGGACTCACACTGATCTCCATCTTTGAGATAGGTT	2573
	GGCAGTTGCAAGGATGA	2574
	TCATCCTTGCAACTGCC	2575
Haemophilia B Asp64Glu GATg-GAG	TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT GGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG TGTCCTTTGGATTTGAAGGAAAGAACTGTGAATTA	2576
	TAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGA	2577
	TGCAAGGATGACATTAA	2578
	TTAATGTCATCCTTGCA	2579
Haemophilia B Asp64Gly GAT-GGT	ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAA TGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTG GTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATT	2580
	AATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACAT CATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGAT	2581

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTGCAAGGATGACATTA	2582
	TAATGTCATCCTTGCAA	2583
Haemophilia B Asp64Asn gGAT-AAT	TATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAA ATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTG GTGTCCCTTTGGATTGAAGGAAAGAACTGTGAAT	2584
	ATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACATTC ATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTAAACAT GGATTGGACTCACACTGATCTCCATCTTTGAGATA	2585
	GTTGCAAGGATGACATT	2586
	AATGTCATCCTTGCAAC	2587
Haemophilia B Ile66Ser ATT-AGT	AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAA	2588
	TTACCTAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT	2589
	GGATGACATTAATTCCT	2590
	AGGAATTAATGTCATCC	2591
Haemophilia B Ile66Thr ATT-ACT	AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAA	2592
	TTACCTAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT	2593
	GGATGACATTAATTCCT	2594
	AGGAATTAATGTCATCC	2595
Haemophilia B Asn67Lys AAT-AAA	TGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAG TTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTT GGATTGAAGGAAAGAACTGTGAATTAGGTAAGTAA	2596
	TTACTTACCTAATTCACAGTTCTTTCTTCAAATCCAAAGGGAC ACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCC ATTTAAACATGGATTGGACTCACACTGATCTCCA	2597
	GACATTAATTCCTATGA	2598
	TCATAGGAATTAATGTC	2599
Haemophilia B Tyr69Cys TAT-TGT	ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATT TGAAGGAAAGAACTGTGAATTAGGTAAGTAAGTAAT	2600
	AATAGTTACTTACCTAATTCACAGTTCTTTCTTCAAATCCAA GGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTG CCGCCATTAAACATGGATTGGACTCACACTGAT	2601

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATTCCTATGAATGTT	2602
	AACATTCATAGGAATTA	2603
Haemophilia B Cys71Term TGT-t-TGA	TGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAGAAGTGTGAATTAGGTAAGTAACTATTTTTTGAA	2604
	TTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCA	2605
	TATGAATGTTGGTGTCC	2606
	GGACACCAACATTCATA	2607
Haemophilia B Cys71Ser TGT-TCT	GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAGAAGTGTGAATTAGGTAAGTAACTATTTTTTGA	2608
	TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCAC	2609
	CTATGAATGTTGGTGTCC	2610
	GACACCAACATTCATAG	2611
Haemophilia B Cys71Tyr TGT-TAT	GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAGAAGTGTGAATTAGGTAAGTAACTATTTTTTGA	2612
	TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCAC	2613
	CTATGAATGTTGGTGTCC	2614
	GACACCAACATTCATAG	2615
Haemophilia B Cys71Ser aTGT-AGT	TGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAGAAGTGTGAATTAGGTAAGTAACTATTTTTTG	2616
	CAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA	2617
	CCTATGAATGTTGGTGT	2618
	ACACCAACATTCATAGG	2619
Haemophilia B Trp72Arg tTGG-AGG	GAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAGAAGTGTGAATTAGGTAAGTAACTATTTTTTGAAT	2620
	ATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTC	2621

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGAATGT <u>I</u> GGTGTCCC	2622
	GGGACACCA <u>A</u> CATTTCAT	2623
Haemophilia B Trp72Term TGGt-TGA	GTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACAT TAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAG AACTGTGAATTAGGTAAGTAACTATTTTTTGAATAC	2624
	GTATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTT CAAATCCAAAGGGACAC <u>C</u> CAACATTCATAGGAATTAATGTCATC CTTGCAACTGCCGCCATTAAACATGGATTGGAC	2625
	GAATGTTGGTGTCCCTT	2626
	AAGGGACAC <u>C</u> CAACATTC	2627
Haemophilia B Cys73Tyr TGT-TAT	CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAA TTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAGAAC TGTGAATTAGGTAAGTAACTATTTTTTGAATACTC	2628
	GAGTATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCT TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTAAACATGGATTGG	2629
	ATGTTGGTGTCCCTTTG	2630
	CAAAGGGAC <u>C</u> CAACAT	2631
Haemophilia B Cys73Arg gTGT-CGT	TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTGAATACT	2632
	AGTATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCT TCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCAT CCTTGCAACTGCCGCCATTAAACATGGATTGGA	2633
	AATGTTGGTGTCCCTTT	2634
	AAAGGGAC <u>C</u> CAACATT	2635
Haemophilia B Cys73Phe TGT-TTT	CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAA TTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAGAAC TGTGAATTAGGTAAGTAACTATTTTTTGAATACTC	2636
	GAGTATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCT TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTAAACATGGATTGG	2637
	ATGTTGGTGTCCCTTTG	2638
	CAAAGGGAC <u>C</u> CAACAT	2639
Haemophilia B Cys73Term TGTc-TGA	CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAA TCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGAAAGAACT GTGAATTAGGTAAGTAACTATTTTTTGAATACTCA	2640
	TGAGTATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTC CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTC ATCCTTGCAACTGCCGCCATTAAACATGGATTG	2641
	TGTTGGTGTCCCTTTG	2642

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAAAGGGACACCAACA	2643
Haemophilia B Gly76Val GGA-GTA	GTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGA ATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTA GGTAAGTAACTATTTTTTTGAATACTCATGGTTCAA	2644
	TTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACA GTTCTTTCCTTCAAATCCAAAGGGACACCAACATTTCATAGGAA TTAATGTCATCCTTGCAACTGCCGCCATTTA AAC	2645
	TCCCTTTGGATTTGAAG	2646
	CTTCAAATCCAAAGGGA	2647
Haemophilia B Gly76Arg tGGA-AGA	TGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATG AATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATT AGGTAAGTAACTATTTTTTTGAATACTCATGGTTCA	2648
	TGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACAG TTCTTTCCTTCAAATCCAAAGGGACACCAACATTTCATAGGAAT TAATGTCATCCTTGCAACTGCCGCCATTTAACA	2649
	GTCCCTTTGGATTTGAA	2650
	TTCAAATCCAAAGGGAC	2651
Haemophilia B Phe77Cys TTT-TGT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTTTGAATACTCATGGTTCAAAGT	2652
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2653
	CTTTGGATTTGAAGGAA	2654
	TTCCTTCAAATCCAAAG	2655
Haemophilia B Phe77Ser TTT-TCT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTTTGAATACTCATGGTTCAAAGT	2656
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2657
	CTTTGGATTTGAAGGAA	2658
	TTCCTTCAAATCCAAAG	2659
Haemophilia B Phe77Tyr TTT-TAT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTTTGAATACTCATGGTTCAAAGT	2660
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2661
	CTTTGGATTTGAAGGAA	2662

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTCCTTCAAATCCAAAG	2663
Haemophilia B Glu78Lys tGAA-AAA	AATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT GGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAA GTAACATTTTTTTGAATACTCATGGTTCAAAGTTT	2664
	AACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAAT TCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCAT AGGAATTAATGTCATCCTTGCAACTGCCGCCATT	2665
	TTGGATTTGAAGGAAAG	2666
	CTTTCCTTCAAATCCAA	2667
Haemophilia B Gly79Val GGA-GTA	GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTA ACTATTTTTTTGAATACTCATGGTTCAAAGTTTCCCT	2668
	AGGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC	2669
	ATTGAAGGAAAGAACT	2670
	AGTTCTTTCCTTCAAAT	2671
Haemophilia B Gly79Arg aGGA-AGA	GGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG TGTCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGT AACTATTTTTTTGAATACTCATGGTTCAAAGTTTCCC	2672
	GGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACC TAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTCATCCTTGCAACTGCCGCC	2673
	GATTTGAAGGAAAGAAC	2674
	GTTCTTTCCTTCAAATC	2675
Haemophilia B Gly79Glu GGA-GAA	GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTA ACTATTTTTTTGAATACTCATGGTTCAAAGTTTCCCT	2676
	AGGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC	2677
	ATTGAAGGAAAGAACT	2678
	AGTTCTTTCCTTCAAAT	2679
Haemophilia B Cys88Ser TGT-TCT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2680
	ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAATA GACAGTAACAGCATCATTTAACATGCATTCTAA	2681
	TGTAACATGTAACATTA	2682

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATGTTACATGTTACA	2683
Haemophilia B Cys88Phe TGT-TTT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2684
	ACCACCTTGTTATCAGCACTATTTTACAAAACCTGCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2685
	TGTAACATGTAACATTA	2686
	TAATGTTACATGTTACA	2687
		2688
Haemophilia B Cys88Arg aTGT-CGT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCT TCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGG	2688
	CCACCTTGTTATCAGCACTATTTTACAAAACCTGCTCGCATCT GCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2689
	ATGTAACATGTAACATT	2690
	AATGTTACATGTTACAT	2691
		2692
Haemophilia B Cys88Tyr TGT-TAT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2692
	ACCACCTTGTTATCAGCACTATTTTACAAAACCTGCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2693
	TGTAACATGTAACATTA	2694
	TAATGTTACATGTTACA	2695
		2696
Haemophilia B Ile90Thr ATT-ACT	ATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTA GATGTAACATGTAACATTAAGAATGGCAGATGCGAGCAGTTTT GTAAAAATAGTGCTGATAACAAGGTGGTTTGCTC	2696
	GAGCAAACCACCTTGTTATCAGCACTATTTTACAAAACCTGCT CGCATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAG CAAATAGACAGTAACAGCATCATTTAACATGCAT	2697
	ATGTAACATTAAGAATG	2698
	CATTCTTAATGTTACAT	2699
		2700
Haemophilia B Asn92His gAAT-CAT	TGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGT AACATGTAACATTAAGAATGGCAGATGCGAGCAGTTTTGTAA AATAGTGCTGATAACAAGGTGGTTTGCTCCTGTA	2700
	TACAGGAGCAAACCACCTTGTTATCAGCACTATTTTACAAAA CTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTAAAA GAAGCAAATAGACAGTAACAGCATCATTTAACA	2701
	ACATTAAGAATGGCAGA	2702
		2702

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TCTGCCAT <u>I</u> CTTAATGT	2703
Haemophilia B Asn92Lys AATg-AAA	TTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAA CATGTAACATTAAGAATGGCAGATGCGAGCAGTTTGTAAAAA TAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT	2704
	AGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTACAA AACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTA AAAGAAGCAAATAGACAGTAACAGCATCATTAA	2705
	ATTAAGAATGGCAGATG	2706
	CATCTGCCATTCTTAAT	2707
Haemophilia B Gly93Asp GGC-GAC	AAATGATGCTGTTACTGTCTATTTTGCTTCTTTAGATGTAACA TGTAACATTAAGAATGGCAGATGCGAGCAGTTTGTAAAAATA GTGCTGATAACAAGGTGGTTTGCTCCTGTACTGA	2708
	TCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTAC AAACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCT AAAGAAGCAAATAGACAGTAACAGCATCATT	2709
	TAAGAATGGCAGATGCG	2710
	CGCATCTGCCATTCTTA	2711
Haemophilia B Gly93Ser tGGC-AGC	TAAATGATGCTGTTACTGTCTATTTTGCTTCTTTAGATGTAAC ATGTAACATTAAGAATGGCAGATGCGAGCAGTTTGTAAAAAT AGTGCTGATAACAAGGTGGTTTGCTCCTGTACTG	2712
	CAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTACA AAACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTA AAAGAAGCAAATAGACAGTAACAGCATCATTTA	2713
	TTAAGAATGGCAGATGC	2714
	GCATCTGCCATTCTTAA	2715
Haemophilia B Arg94Ser AGAt-AGT	GATGCTGTTACTGTCTATTTTGCTTCTTTAGATGTAACATGTA ACATTAAGAATGGCAGATGCGAGCAGTTTGTAAAAATAGTGC TGATAACAAGGTGGTTTGCTCCTGTACTGAGGGA	2716
	TCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTT TTACAAAAGTCTCGCATCTGCCATTCTTAATGTTACATGTTAC ATCTAAAAGAAGCAAATAGACAGTAACAGCATC	2717
	AATGGCAGATGCGAGCA	2718
	TGCTCGCATCTGCCATT	2719
Haemophilia B Cys95Tyr TGC-TAC	TGCTGTTACTGTCTATTTTGCTTCTTTAGATGTAACATGTAAC ATTAAGAATGGCAGATGCGAGCAGTTTGTAAAAATAGTGCTG ATAACAAGGTGGTTTGCTCCTGTACTGAGGGATA	2720
	TATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTAT TTTTACAAAAGTCTCGCATCTGCCATTCTTAATGTTACATGTT ACATCTAAAAGAAGCAAATAGACAGTAACAGCA	2721
	TGGCAGATGCGAGCAGT	2722

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGCTCGCATCTGCCA	2723
Haemophilia B Cys95Trp TGCg-TGG	GCTGTTACTGTCTATTTTGCTTCTTTAGATGTAACATGTAACA TTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGA TAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT	2724
	ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTA TTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGT TACATCTAAAAGAAGCAAATAGACAGTAACAGC	2725
	GGCAGATGCGAGCAGTT	2726
	AACTGCTCGCATCTGCC	2727
Haemophilia B Cys95Term TGCg-TGA	GCTGTTACTGTCTATTTTGCTTCTTTAGATGTAACATGTAACA TTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGA TAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT	2728
	ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTA TTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGT TACATCTAAAAGAAGCAAATAGACAGTAACAGC	2729
	GGCAGATGCGAGCAGTT	2730
	AACTGCTCGCATCTGCC	2731
Haemophilia B Gln97Pro CAG-CCG	TACTGTCTATTTTGCTTCTTTAGATGTAACATGTAACATTAAG AATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACA AGGTGGTTTGCTCCTGTACTGAGGGATATCGACT	2732
	AGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCA GCACTATTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTT ACATGTTACATCTAAAAGAAGCAAATAGACAGTA	2733
	ATGCGAGCAGTTTTGT	2734
	TACAAAACCTGCTCGCAT	2735
Haemophilia B Gln97Glu gCAG-GAG	TACTGTCTATTTTGCTTCTTTAGATGTAACATGTAACATTAA GAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAAC AAGGTGGTTTGCTCCTGTACTGAGGGATATCGAC	2736
	GTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAG CACTATTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTA CATGTTACATCTAAAAGAAGCAAATAGACAGTAA	2737
	GATGCGAGCAGTTTTGT	2738
	ACAAAACCTGCTCGCATC	2739
Haemophilia B Cys99Arg tTGT-CGT	TCTATTTTGCTTCTTTAGATGTAACATGTAACATTAAAGAATGG CAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTG GTTTGCTCCTGTACTGAGGGATATCGACTTGCAG	2740
	CTGCAAGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGT TATCAGCACTATTTTACAAAACCTGCTCGCATCTGCCATTCTT AATGTTACATGTTACATCTAAAAGAAGCAAATAGA	2741
	AGCAGTTTTGTAAAAAT	2742

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATTTTACAAACTGCT	2743
Haemophilia B Cys99Tyr TGT-TAT	CTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGC AGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTG GTTTGCTCCTGTACTGAGGGATATCGACTTGCAGA	2744
	TCTGCAAGTCGATATCCCTCAGTACAGGAGCAAACACCTTG TTATCAGCACTATTTTACAAACTGCTCGCATCTGCCATTCTT AATGTTACATGTTACATCTAAAAGAAGCAAATAG	2745
	GCAGTTTTGTAAAAATA	2746
	TATTTTACAAACTGC	2747
Warfarin sensitivity Ala(-10)Thr cGCC-ACC	TTTTTGCTAAACTAAAGAATTATTCTTTACATTTAGTTTT CTTGATCATGAAAACGCCAACAAATTCTGAATCGGCCAAAGA GGTATAATTCAGGTAAATTGGAAGAGTTTGTTT	2748
	GAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCG ATTCAGAATTTTGTGGCGTTTTCATGATCAAGAAAACTGAAA TGTAAGAATAATTCTTTAGTTTTCAGCAAAAA	2749
	ATGAAAACGCCAACAAA	2750
	TTTGTTGGCGTTTTCAT	2751
Warfarin sensitivity Ala(-10)Val GCC-GTC	TTTTTGCTAAACTAAAGAATTATTCTTTACATTTAGTTTTT TTGATCATGAAAACGCCAACAAATTCTGAATCGGCCAAAGAG GTATAATTCAGGTAAATTGGAAGAGTTTGTTCA	2752
	TGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCC GATTCAGAATTTTGTGGCGTTTTCATGATCAAGAAAACTGA AATGTAAAGAATAATTCTTTAGTTTTCAGCAAAAA	2753
	TGAAAACGCCAACAAA	2754
	TTTTGTTGGCGTTTTC	2755
Haemophilia B Gly(-26)Val GGA-GTA	TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTAC AGGTTTGTTTCTTTTTTAAATACATTGAGTATGC	2756
	GCATACTCAATGTATTTTAAAAAAGGAAACAAACCTGTACATTC AGCACTGAGTAGATATCTAAAGGCAGATGGTGTGAGGCC TGGTGATTCTGCCATGATCATGTTACGCGCTGCA	2757
	CCTTTTAGGATATCTAC	2758
	GATGATATCTAAAGG	2759
Haemophilia B Leu(-27)Ter TTA-TAA	TTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCC TCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATG TACAGGTTTGTTTCTTTTTTAAATACATTGAGTA	2760
	TACTCAATGTATTTTAAAAAAGGAAACAAACCTGTACATTCAGC ACTGAGTAGATATCTAAAGGCAGATGGTGTGAGGCCTGG TGATTCTGCCATGATCATGTTACGCGCTGCATAA	2761
	CTGCCTTTTAGGATATC	2762

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GATATCCTAAAAGGCAG	2763
Haemophilia B Ile(-30)Asn ATC-AAC	TAGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAAT CACCAGGCCTCATCACCATCTGCCTTTTAGGATATCTACTCAG TGCTGAATGTACAGGTTTGTTCCTTTTTTAAATA	2764
	TATTTTAAAAAAGGAAACAAACCTGTACATTCAGCACTGAGTA GATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCTG CCATGATCATGTTACGCGCTGCATAACCTTTGCTA	2765
	CATCACCATCTGCCTTT	2766
	AAAGGCAGATGGTGATG	2767
Haemophilia B Ile(-40)Phe gATC-TTC	ACTAATCGACCTTACCACTTTCACAATCTGCTAGCAAAGGTTA TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTG	2768
	CAGCACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGC CTGGTGATTCTGCCATGATCATGTTACGCGCTGCATAACCTT TGCTAGCAGATTGTGAAAGTGGTAAGGTCGATTAGT	2769
	TGAACATGATCATGGCA	2770
	TGCCATGATCATGTTCA	2771
Haemophilia B Arg(-44)His CGC-CAC	ACTTTGGTACAATAATCGACCTTACCACTTTCACAATCTGCT AGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATC ACCAGGCCTCATCACCATCTGCCTTTTAGGATATCT	2772
	AGATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCT GCCATGATCATGTTACGCGCTGCATAACCTTTGCTAGCAGA TTGTGAAAGTGGTAAGGTCGATTAGTTGTACCAAAGT	2773
	TATGCAGCGCGTGAACA	2774
	TGTTACGCGCTGCATA	2775

EXAMPLE 15**Alpha thalassemia - Hemoglobin alpha locus 1**

The thalassemia syndromes are a heterogeneous group of inherited anemias characterized by defects in the synthesis of one or more globin chain subunits. For example, beta-thalassemia discussed in Example 6, is caused by a decrease in beta-chain production relative to alpha-chain production; the converse is the case for alpha-thalassemia. The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 1 oligonucleotides of the invention.

Table 22
HBA1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Met(-1)Val cATG-GTG	CCCTGGCGCGCTCGCGGCCCGGCACTCTTCTGGTCCCCACA GACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACA AGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGC	2776
	GCGCGCCGACCTTACCCAGGCGGCCCTTGACGTTGGTCTTG TCGGCAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGT GGGGACCAGAAGAGTGCCGGGCGCGAGCGCGCCAGGG	2777
	AACCCACCATGGTGCTG	2778
	CAGCACCATGGTGGGTT	2779
Haemoglobin variant Ala12Asp GCC-GAC	CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCC GACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGC GCACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG	2780
	CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCAGGCGGCCCTTGACGTTGGTCTTGTCGG CAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGTG	2781
	CGTCAAGGCCGCCTGGG	2782
	CCCAGGCGGCCCTTGACG	2783
Haemoglobin variant Gly15Asp GGT-GAT	AGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCA ACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCT	2784
	AGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCC AGCGTGCGCGCCGACCTTACCCAGGCGGCCCTTGACGTTGG TCTTGTCGGCAGGAGACAGCACCATGGTGGGTTCTCTCT	2785
	CGCCTGGGGTAAGGTGCG	2786
	CGACCTTACCCAGGCG	2787
Haemoglobin variant Tyr24Cys TAT-TGT	CTGCCGACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTC GGCGCGCACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGA GGTGAGGCTCCCTCCCCTGCTCCGACCCGGGCTCCTCGCC	2788
	GGCGAGGAGCCCGGGTCCGAGCAGGGGAGGGAGCCTCACC TCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGCGCCG ACCTTACCCAGGCGGCCCTTGACGTTGGTCTTGTCGGCAG	2789
	TGGCGAGTATGGTGCGG	2790
	CCGCACCATACTCGCCA	2791
Haemoglobin variant Glu27Asp GAGg-GAT	GACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGAC C	2792
	GGTCCGGGCGGGCGAGGAGCCCGGGTCCGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCAGGCGGCCCTTGACGTTGGTC	2793
	GGTGCGGAGGCCCTGGA	2794
	TCCAGGGCCTCCGCACC	2795

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemoglobin variant Asn68Lys AACg-AAG	GAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2796
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATG TCGTCCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCAC CTTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2797
	CTGACCAACGCCGTGGC	2798
	GCCACGGCGTTGGTCAG	2799
Haemoglobin variant Asp74Gly GAC-GGC	AGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACC AACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCTGTC CGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGGA	2800
	TCCACCCGAAGCTTGTGCGCGTGCAGGTGCTCAGGGCGGA CAGCGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGG TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCT	2801
	GCACGTGGACGACATGC	2802
	GCATGTCGTCCACGTGC	2803
Haemoglobin variant Asp74His gGAC-CAC	CAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGAC CAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCTGT CCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG	2804
	CCACCCGAAGCTTGTGCGCGTGCAGGTGCTCAGGGCGGAC AGCGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT CAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTG	2805
	CGCACGTGGACGACATG	2806
	CATGTCGTCCACGTGCG	2807
Haemoglobin variant Asn78His cAAC-CAC	CACGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGG CGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGC GACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACT	2808
	AGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCG CTCAGGGCGGACAGCGCGTGGGCATGTCGTCCACGTGCGC CACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCGTG	2809
	ACATGCCCAACGCGCTG	2810
	CAGCGCGTTGGGCATGT	2811
Haemoglobin variant His87Tyr gCAC-TAC	ACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCT GTCCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG ACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGGAGCGA	2812
	TCGCTCCCGGCCCGCCGCTCACCTTGAAGTTGACCGGGTCC ACCCGAAGCTTGTGCGCGTGCAGGTGCTCAGGGCGGACAG CGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT	2813
	GCGACCTGCACGCGCAC	2814
	GTGCGCGTGCAGGTGCG	2815
Haemoglobin variant Lys90Asn AAGc-AAC	GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTGAG	2816

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC	2817
	GCGCACAAGCTTCGGGT	2818
	ACCCGAAGCTTGTGCGC	2819
Haemoglobin variant Lys90Thr AAG-ACG	TGGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTG AGCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAA CTTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTGCA	2820
	TCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGTT GACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCA GGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCCA	2821
	CGCGCACAAGCTTCGGG	2822
	CCCGAAGCTTGTGCGCG	2823
Haemoglobin variant Arg92Gln CGG-CAG	ACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGAC CTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAA GGTGAGCGGCGGGCCGGGAGCGATCTGGGTGAGGGGGC	2824
	CGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTT GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGT	2825
	CAAGCTTCGGGTGGACC	2826
	GGTCCACCCGAAGCTTG	2827
Haemoglobin variant Asp94Gly GAC-GGC	ACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCAC GCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAG CGGCGGGCCGGGAGCGATCTGGGTGAGGGGGCGAGATGG	2828
	CCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCT CACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGT GCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGTCGT	2829
	TCGGGTGGACCCGGTCA	2830
	TGACCGGGTCCACCCGA	2831
Haemoglobin variant Pro95Arg CCG-CGG	ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTGAGGGGGCGAGATGGCGC	2832
	GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT	2833
	GGTGGACCCGGTCAACT	2834
	AGTTGACCGGGTCCACC	2835
Haemoglobin variant Ser102Arg AGCc-AGA	CGGCGGCTGCGGGCCTGGGCCCTCGGCCCCACTGACCCTC TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG GCCGCCACCTCCCCGCCGAGTTACCCCTGCGGTGCAC	2836
	GTGCACCGCAGGGGTGAAGTTCGGCGGGGAGGTGGGCGGCC AGGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAA GAGGGTCAGTGGGGCCGAGGGCCAGGCCCGCAGCCGCCG	2837
	CTCCTAAGCCACTGCCT	2838

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AGGCAGTGGCTTAGGAG	2839
Haemoglobin variant Glu116Lys cGAG-AAG	TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG	2840
	GCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGC	
	CTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGC	
	GCACGGTGCTCACAGAAGCCAGGAAGTGTCCAGGGAGGCG	2841
	TGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCCA	
	GGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAA	
	TCCCCGCCGAGTTCACC	2842
	GGTGAAGTGGCGGGGA	2843
Haemoglobin variant Ala120Glu GCG-GAG	TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTC	2844
	CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA	
	GTTCTTGGCTTCTGTGAGCACCGTGCTGACCTCCAAATA	
	TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAAGTTG	2845
	TCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGA	
	GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA	
	CACCCCTGCGGTGCACG	2846
	CGTGCACCGCAGGGGTG	2847
Thalassaemia alpha Leu129Pro CTG-CCG	TGGCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC	2848
	GCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCTG	
	ACCTCCAAATACCGTTAAGCTGGAGCCTCGGTGGCCAT	
	ATGGCCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGC	2849
	ACGGTGCTCACAGAAGCCAGGAAGTGTCCAGGGAGGCGTG	
	CACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCCA	
	CAAGTTCCTGGCTTCTG	2850
	CAGAAGCCAGGAAGTTG	2851
Haemoglobin variant Arg141Leu CGT-CTT	TGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCG	2852
	TGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTGGCCA	
	TGCTTCTTGCCCCTTGGGCCTCCCCCAGCCCCCTCCT	
	AGGAGGGGCTGGGGGGAGGCCCAAGGGGCAAGAAGCATGG	2853
	CCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACG	
	GTGCTCACAGAAGCCAGGAAGTGTCCAGGGAGGCGTGCA	
	CAAATACCGTTAAGCTG	2854
	CAGCTTAACGGTATTTG	2855

EXAMPLE 16**Alpha-thalassemia - Hemoglobin alpha locus 2**

The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 2 oligonucleotides of the invention.

Table 23
HBA2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Met(-1)Thr ATG-ACG	CCTGGCGCGCTCGCGGGCCGGCACTCTTCTGGTCCCCACAG ACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAG ACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCA	2856
	TGCGCGCCGACCTTACCCAGGCGGCCTTGACGTTGGTCTT GTCGGCAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCT GTGGGGACCAGAAGAGTGCCGGCCCGCGAGCGCGCCAGG	2857
	ACCCACCATGGTGCTGT	2858
	ACAGCACCATGGTGGGT	2859
Haemoglobin variant Ala12Asp GCC-GAC	CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCC GACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGC GCACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG	2860
	CACCTCTCCAGGGCCTCCGCACCATCTCGCCAGCGTGCGC GCCGACCTTACCCAGGCGGCCTTGACGTTGGTCTTGTCTCGG CAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGTG	2861
	CGTCAAGGCCGCCTGGG	2862
	CCCAGGCGGCCTTGACG	2863
Haemoglobin variant Lys16Glu tAAG-GAG	AGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCAAC GTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCACGCTGGCG AGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC	2864
	GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATCTCG CCAGCGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGTT GGTCTTGTCTCGGAGGAGACAGCACCATGGTGGGTTCTCT	2865
	CCTGGGGTAAGGTCGGC	2866
	GCCGACCTTACCCAGG	2867
Haemoglobin variant His20Gln CACg-CAA	GGTGCTGTCTCCTGCCGACAAGACCAACGTCAAGGCCGCCT GGGGTAAGGTCGGCGCGCACGCTGGCGAGTATGGTGCGGA GGCCCTGGAGAGGTGAGGCTCCCTCCCCTGCTCCGACCCG	2868
	CGGGTCGGAGCAGGGGAGGGAGCCTCACCTCTCCAGGGCC TCCGCACCATCTCGCCAGCGTGCGCGCCGACCTTACCCCA GGCGGCCTTGACGTTGGTCTTGTCTGGCAGGAGACAGCACC	2869
	GGCGCGCAGGCTGGCGA	2870
	TCGCCAGCGTGCGCGCC	2871
Haemoglobin variant Glu27Asp GAGg-GAC	GACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGAC C	2872
	GGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGCCTCCGCACCATCTCGCCAG CGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGTTGGTC	2873
	GGTGCGGAGGCCCTGGA	2874
	TCCAGGGCCTCCGCACC	2875

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Leu29Pro CTG-CCG	ACGTCAAGGCCGCTGGGGTAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC CCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGACCCACAG	2876
	CTGTGGGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGG GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGT GGAGGCCCTGGAGAGGT	2877
	ACCTCTCCAGGGCCTCC	2878
		2879
Haemoglobin variant Asp47His cGAC-CAC	GCTTCTCCCCGCAGGATGTTCTGTCTTCCCCACCACCAAG ACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCCA GGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGA	2880
	TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTGG GCAGAGCCGTGGCTCAGGTGGAAGTGCGGGAAGTAGGTCTT GGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAGAAGC	2881
	CGCACTTCGACCTGAGC	2882
	GCTCAGGTGGAAGTGCG	2883
Haemoglobin variant Leu48Arg CTG-CGG	CTCCCCGCAGGATGTTCTGTCTTCCCCACCACCAAGACCT ACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCAGGTTA AGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACCAA	2884
	TTGGTCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAAC CTGGGCAGAGCCGTGGCTCAGGTGGAAGTGCGGGAAGTAG GTCTTGGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAG	2885
	CTTCGACCTGAGCCACG	2886
	CGTGGCTCAGGTGGAAG	2887
Haemoglobin variant Gln54Glu cCAG-GAG	CTGTCTTCCCCACCACCAAGACCTACTTCCCGCACTTCGAC CTGAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAA GGTGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGG	2888
	CCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCACCTTC TTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTCAGGTC GAAGTGCGGGAAGTAGGTCTTGGTGGTGGGGAAGGACAG	2889
	GCTCTGCCAGGTTAAG	2890
	CTTAACCTGGGCAGAGC	2891
Haemoglobin variant Gly59Asp GGC-GAC	CCAAGACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTG CCCAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCT GACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGC	2892
	GCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAG CGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTGGGCAG AGCCGTGGCTCAGGTCGAAGTGCGGGAAGTAGGTCTTGG	2893
	GGGCCACGGCAAGAAGG	2894
	CCTTCTTGCCGTGGCCC	2895
Haemoglobin variant Asn68Lys AACg-AAG	GAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGGACGA CATGCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2896

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATG TCGTCCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCAC CTTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2897
	CTGACCAACGCCGTGGC	2898
	GCCACGGCGTTGGTCAG	2899
Haemoglobin variant Asn68Lys AACg-AAA	GAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2900
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATG TCGTCCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCAC CTTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2901
	CTGACCAACGCCGTGGC	2902
	GCCACGGCGTTGGTCAG	2903
Haemoglobin variant Asn78Lys AACg-AAA	CGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGGCG CACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGA CCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACTTC	2904
	GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGC GCCACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCG	2905
	ATGCCCAACGCGCTGTC	2906
	GACAGCGCGTTGGGCAT	2907
Haemoglobin variant Asp85Val GAC-GTC	CGCTGACCAACGCCGTGGCGCACGTGGACGACATGCCCAAC GCGCTGTCCGCCCTGAGCGACCTGCACGCGCACAAGCTTCG GGTGGACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGG	2908
	CCCGGCCCGCGCTCACCTTGAAGTTGACCGGGTCCACCCG AAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGACAGCGCGT TGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAGCG	2909
	CCTGAGCGACCTGCACG	2910
	CGTGCAGGTCGCTCAGG	2911
Haemoglobin variant Lys90Asn AAGc-AAT	GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAG	2912
	CTCGACCCAGATCGCTCCCGGCCCGCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC	2913
	GCGCACAAGCTTCGGGT	2914
	ACCCGAAGCTTGTGCGC	2915
Haemoglobin variant Asp94His gGAC-CAC	GACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCA CGCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGA GCGGCGGGCCGGGAGCGATCTGGGTCGAGGGGCGAGATG	2916
	CATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCGCTC ACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTG CAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTC	2917
	TTCCGGGTGGACCCGGTC	2918

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GACCGGGTCCACCCGAA	2919
Haemoglobin variant Pro95Leu CCG-CTG	ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATGGCGC	2920
	GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGT	2921
	GGTGGACCCGGTCAACT	2922
	AGTTGACCGGGTCCACC	2923
Haemoglobin variant Ser102Arg aAGC-CGC	TAGCGCAGGCGGGCGGCTGCGGGCCTGGGCGCACTGACCC TCTTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCC TGGCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGC	2924
	GCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCCAG GGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAAGA GGGTCAGTGCGGCCAGGCCCGCAGCCGCCGCTGCGCTA	2925
	AGCTCCTAAGCCACTGC	2926
	GCAGTGGCTTAGGAGCT	2927
Haemoglobin H disease Cys104Tyr TGC-TAC	GGCGGCGGCTGCGGGCCTGGGCGCACTGACCCTCTTCTCT GCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGC CCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC	2928
	GAGGCGTGACCCGAGGGGTGAACTCGGCGGGGAGGTGGG CGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCA GAGAAGAGGGTCAGTGCGGCCAGGCCCGCAGCCGCCGCC	2929
	AAGCCACTGCCTGCTGG	2930
	CCAGCAGGCAGTGGCTT	2931
Haemoglobin variant Ala111Val GCC-GTC	CCGCACTGACCCTCTTCTCTGCACAGCTCCTAAGCCACTGCC TGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTC	2932
	GAAGCCAGGAAGTGTCCAGGGAGGCGTGCACCGCAGGGGT GAACTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGG CAGTGGCTTAGGAGCTGTGCAGAGAAGAGGGTCAGTGCGG	2933
	CCTGGCCGCCACCTCC	2934
	GGAGGTGGGCGGCCAGG	2935
Haemoglobin variant Ala120Glu GCG-GAG	TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCTTGGCTTCTGTGAGCACCCTGCTGACCTCCAATA	2936
	TATTTGGAGGTGAGCAGCGGTGCTCACAGAAGCCAGGAACTTG TCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA	2937
	CACCCCTGCGGTGCACG	2938
	CGTGCACCGCAGGGGTG	2939
Haemoglobin variant His122Gln CACg-CAG	CCACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCG AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCCTGCTGACCTCCAATACCGTTAA	2940

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGG CGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTGG	2941
	GCGGTGCACGCCTCCCT	2942
	AGGGAGGCGTGCACCGC	2943
Haemoglobin variant Ala123Ser cGCC-TCC	CACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCGA GTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGG CTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAG	2944
	CTTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCA GGAATTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTCG GCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTG	2945
	CGGTGCACGCCTCCCTG	2946
	CAGGGAGGCGTGCACCG	2947
Thalassaemia alpha Leu125Pro CTG-CCG	TGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGT GAGCACCGTGCTGACCTCCAAATACCGTTAAGCTGGAGC	2948
	GCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGTGCTCACA GAAGCCAGGAAGTTGTCCAGGGAGGCGTGCACCGCAGGGG TGAAGTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCA	2949
	CGCCTCCCTGGACAAGT	2950
	ACTTGTCCAGGGAGGCG	2951
Haemoglobin variant Ser131Pro TCT-CCT	GCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC CCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCTGACCTC CAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCTCTC	2952
	GAGGAACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAG GTCAGCACGGTGCTCACAGAAGCCAGGAAGTTGTCCAGGGA GGCGTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGC	2953
	TCCTGGCTTCTGTGAGC	2954
	GCTCACAGAAGCCAGGA	2955
Haemoglobin variant Leu136Met gCTG-ATG	GAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCT GGCTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAGC TGGAGCCTCGGTAGCCGTTCTCTCTGTCGCTGGGCCT	2956
	AGGCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAGC TTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTC	2957
	GCACCGTGCTGACCTCC	2958
	GGAGGTCAGCACGGTGC	2959
Haemoglobin variant Leu136Pro CTG-CCG	AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAGCT GGAGCCTCGGTAGCCGTTCTCTCTGCCCGCTGGGCCTC	2960
	GAGGCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAG CTTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCA GGAATTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACT	2961
	CACCGTGCTGACCTCCA	2962

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGGAGGTCAGCACGGTG	2963
Haemoglobin variant Arg141Cys cCGT-TGT	GTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACC	2964
	GTGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCC	
	GTTCCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCC	
	GGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGAACGGC	2965
	TACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGT	
	GCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCGTGCAC	
	CCAAATACCGTTAAGCT	2966
	AGCTTAACGGTATTTGG	2967
Haemoglobin variant Term142Gln tTAA-CAA	CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG	2968
	CTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTT	
	CCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCC	
	GGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGAAC	2969
	GGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCA	
	CGGTGCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCGTG	
	AATACCGTTAAGCTGGA	2970
	TCCAGCTTAACGGTATT	2971
Haemoglobin variant Term142Lys tTAA-AAA	CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG	2972
	CTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTT	
	CCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCC	
	GGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGAAC	2973
	GGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCA	
	CGGTGCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCGTG	
	AATACCGTTAAGCTGGA	2974
	TCCAGCTTAACGGTATT	2975
Haemoglobin variant Term142Tyr TAAg-TAT	CGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCT	2976
	GACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCC	
	TCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCCCC	
	GGGGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGG	2977
	AACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAG	
	CACGGTGCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCG	
	TACCGTTAAGCTGGAGC	2978
	GCTCCAGCTTAACGGTA	2979

EXAMPLE 17
Human mismatch repair - MLH1

The human MLH1 gene is homologous to the bacterial *mutL* gene, which is involved in mismatch repair. Mutations in the MLH1 gene have been identified in many individuals with hereditary nonpolyposis colorectal cancer (HNPCC). Mutations in the MLH1 gene are also implicated in predisposition to a variety of cancers associated with, for example, Muir-Torre syndrome and Turcot

syndrome. The attached table discloses the correcting oligonucleotide base sequences for the MLH1 oligonucleotides of the invention.

Table 24
MLH1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Met1Arg ATG-AGG	TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTCTGTCGAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC	2980
	GCCGCGATGCGGTTCACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA	2981
	CGCCAAAATGTCGTTG	2982
	CGAACGACATTTTGGCG	2983
Non-polyposis colorectal cancer Met1Lys ATG-AAG	TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTCTGTCGAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC	2984
	GCCGCGATGCGGTTCACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA	2985
	CGCCAAAATGTCGTTG	2986
	CGAACGACATTTTGGCG	2987
Non-polyposis colorectal cancer Met35Arg ATG-AGG	TGGTGAACCGCATCGCGGCGGGGAAGTTATCCAGCGGCCA GCTAATGCTATCAAAGAGATGATTGAGAACTGGTACGGAGGG AGTCGAGCCGGGCTCACTTAAGGGCTACGACTTAACGG	2988
	CCGTAAAGTCGTAGCCCTTAAGTGAAGCCGGCTCGACTCCCT CCGTACCAAGTTCTCAATCATCTCTTTGATAGCATTAGCTGGCC GCTGGATAACTTCCCCCGCCGCGATGCGGTTACCA	2989
	CAAAGAGATGATTGAGA	2990
	TCTCAATCATCTCTTG	2991
Non-polyposis colorectal cancer Ser44Phe TCC-TTC	TAGAGTAGTTGCAGACTGATAAATTATTTCTGTTTGATTGCG AGTTTAGATGCAAAATCCACAAGTATTCAAGTGATTGTTAAAG AGGGAGGCCTGAAGTTGATTCAGATCCAAGACAA	2992
	TTGTCTTGGATCTGATCAACTTCAGGCCTCCCTCTTTAACAA TCACTTGAATACTTGTGGATTTTGCATCTAACTGGCAAATCA AACAGAAAATAATTTATCAGTCTGCAACTACTCTA	2993
	TGCAAAATCCACAAGTA	2994
	TACTTGTGGATTTTGCA	2995
Non-polyposis colorectal cancer Gln62Lys CAA-AAA	GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTCAGATCCAAAGACAATGGCACCAGGATCAGG GTAAGTAAACCTCAAAGTAGCAGGATGTTTGTGCGC	2996

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGAT CCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCC CTCTTTAACAATCACTTGAATACTTGTGGATTTTGC	2997
	TTCAGATCCAAGACAAT	2998
	ATTGTCTTGGATCTGAA	2999
Non-polypoidis colorectal cancer Gln62Term CAA-TAA	GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTGAGATCCAAGACAATGGCACC G GGATCAGG GTAAGTAAACCTCAAAGTAGCAGGATGTTTGTGCGC	3000
	GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGAT CCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCC CTCTTTAACAATCACTTGAATACTTGTGGATTTTGC	3001
	TTCAGATCCAAGACAAT	3002
	ATTGTCTTGGATCTGAA	3003
Non-polypoidis colorectal cancer Asn64Ser AAT-AGT	CCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGT TGATTGAGATCCAAGACAATGGCACC G GGATCAGGGTAAGTA AAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGG	3004
	CCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTA CCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCA GGCCTCCCTCTTTAACAATCACTTGAATACTTGTGG	3005
	CCAAGACAATGGCACCG	3006
	CGGTGCCATTGTCTTGG	3007
Non-polypoidis colorectal cancer Gly67Arg GGG-AGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAGA TCCAAGACAATGGCACCCGGGATCAGGGTAAGTAAACCTCAA AGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3008
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3009
	ATGGCACCCGGGATCAGG	3010
	CCTGATCCCGGTGCCAT	3011
Non-polypoidis colorectal cancer Gly67Arg GGG-CGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAGA TCCAAGACAATGGCACCCGGGATCAGGGTAAGTAAACCTCAA AGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3012
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3013
	ATGGCACCCGGGATCAGG	3014
	CCTGATCCCGGTGCCAT	3015
Non-polypoidis colorectal cancer Gly67Trp GGG-TGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAGA TCCAAGACAATGGCACCCGGGATCAGGGTAAGTAAACCTCAA AGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3016
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3017
	ATGGCACCCGGGATCAGG	3018

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polypoid colorectal cancer Thr117Arg ACG-AGG	TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGC TCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCA TACAGGTATAGTGCTGACTTCTTTTACTCATATAT	3040
	ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACT TTCCATCAGCTGTTTTCGTTGTAATAGTAACATGAGCCACATG GCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA	3041
	TATTACAACGAAAACAG	3042
	CTGTTTTCTGTTGTAATA	3043
	TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGC TCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCA TACAGGTATAGTGCTGACTTCTTTTACTCATATAT	3044
Non-polypoid colorectal cancer Thr117Met ACG-ATG	ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACT TTCCATCAGCTGTTTTCGTTGTAATAGTAACATGAGCCACATG GCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA	3045
	TATTACAACGAAAACAG	3046
	CTGTTTTCTGTTGTAATA	3047
	TCTATCTCTCTACTGGATATTAATTTGTTATATTTCTCATTAGA GCAAGTTACTCAGATGGAAAAGTGAAGCCCCCTCCTAAACCA TGTGCTGGCAATCAAGGGACCCAGATCACGGTAA	3048
	TTACCGTGATCTGGGTCCCTTGATTGCCAGCACATGGTTTAG GAGGGGCTTTCAGTTTTCCATCTGAGTAAGTTGCTCTAATGAG AAATATAACAAATTAATATCCAGTAGAGAGATAGA	3049
Non-polypoid colorectal cancer Gly133Term GGA-TGA	ACTCAGATGGAAAAGT	3050
	CAGTTTTCCATCTGAGT	3051
	TAGTGTGTGTTTTGGCAACTCTTTTCTTACTCTTTGTTTTTC TTTTCCAGGTATTCAGTACACAATGCAGGCATTAGTTTCTCAG TTAAAAAGTAAGTTCTTGGTTTATGGGGGATGG	3052
	CCATCCCCCATAAACCAAGAACTTACTTTTTTAAGTGAAGAAC TAATGCCTGCATTGTGTACTGAATACCTGGAAAAGAAAAACAA AAGAGTAAGAAAAGAGTTGCCAAAAACACACACTA	3053
	GTATTCAGTACACAATG	3054
Non-polypoid colorectal cancer Val185Gly GTA-GGA	CATTGTGTACTGAATAC	3055
	TTTCTTACTCTTTTGTGTTTTCTTTCCAGGTATTCAGTACACAAT GCAGGCATTAGTTTCTCAGTTAAAAAGTAAGTTCTTGGTTTAT GGGGGATGGTTTTGTTTTATGAAAAGAAAAAA	3056
	TTTTTCTTTTCATAAAACAAAACCATCCCCCATAAACCAAGAA CTTACTTTTTTAAGTGAAGAACTAATGCCTGCATTGTGTACTG AATACCTGGAAAAGAAAAACAAAAGAGTAAGAAA	3057
	TTAGTTTCTCAGTTAAA	3058
	TTTAACTGAGAACTAA	3059
Non-polypoid colorectal cancer Val213Met GTG-ATG	TTTGTTTATCAGCAAGGAGAGACAGTAGCTGATGTTAGGACA CTACCCAATGCCTCAACCGTGGACAATATTCGCTCCATCTTTG GAAATGCTGTTAGTCGGTATGTCGATAACCTATATA	3060

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATATAGGTTATCGACATACCGACTAACAGCATTTCCAAAGAT GGAGCGAATATTGTCCACGGTTGAGGCATTGGGTAGTGTCT AACATCAGCTACTGTCTCTCCTTGCTGATAAACAAA	3061
	CCTCAACCGTGGACAAT	3062
	ATTGTCCACGGTTGAGG	3063
Non-polypoidis colorectal cancer Arg217Cys CGC-TGC	CAAGGAGAGACAGTAGCTGATGTTAGGACACTAC AATGCC TCAACCGTGGACAATATTGGCTCCATCTTTGGAAA JCTGTTA GTCGGTATGTCGATAACCTATATAAAAAAATCTTTT	3064
	AAAAGATTTTTTATATAGGTTATCGACATACCGACTAACAGC TTTCCAAAGATGGAGCGAATATTGTCCACGGTTGAGGCATTG GGTAGTGTCTAACATCAGCTACTGTCTCTCCTTG	3065
	ACAATATTGGCTCCATC	3066
	GATGGAGCGAATATTGT	3067
Non-polypoidis colorectal cancer Ile219Val ATC-GTC	GAGACAGTAGCTGATGTTAGGACACTACCCAATGCCTCAACC GTGGACAATATTGGCTCCATCTTTGGAAATGCTGTTAGTCGGT ATGTCGATAACCTATATAAAAAAATCTTTTACATTT	3068
	AAATGTAAAAGATTTTTTATATAGGTTATCGACATACCGACTA ACAGCATTTCCAAAGATGGAGCGAATATTGTCCACGGTTGAG GCATTGGGTAGTGTCTAACATCAGCTACTGTCTC	3069
	TTCGCTCCATCTTTGGA	3070
	TCCAAAGATGGAGCGAA	3071
Non-polypoidis colorectal cancer Gly244Asp GGT-GAT	CTAATAGAGAACTGATAGAAATTGGATGTGAGGATAAAACCCT AGCCTTCAAATGAATGGTTACATATCCAATGCAAACACTACTCA GTGAAGAAGTGCATCTTCTTACTCTTCATCAACCG	3072
	CGGTTGATGAAGAGTAAGAAGATGCACTTCTTCACTGAGTAG TTTGCATTGGATATGTAACCATTCATTTTGAAGGCTAGGGTTT TATCCTCACATCCAATTTCTATCAGTTCTCTATTAG	3073
	AATGAATGGTTACATAT	3074
	ATATGTAACCATTCAAT	3075
Non-polypoidis colorectal cancer Ser252Term TCA-TAA	GATGTGAGGATAAAACCCTAGCCTTCAAATGAATGGTTACAT ATCCAATGCAAACACTACTCAGTGAAGAAGTGCATCTTCTTACTC TTCATCAACCGTAAGTTAAAAGAACCACATGGGA	3076
	TCCATGTGGTTCTTTTAACTTACGGTTGATGAGAGTAAGA AGATGCACTTCTTCACTGAGTAGTTTGCATTGGATATGTAACC ATTCATTTTGAAGGCTAGGGTTTTATCCTCACATC	3077
	AAACTACTCAGTGAAGA	3078
	TCTTCACTGAGTAGTTT	3079
Non-polypoidis colorectal cancer Glu268Gly GAA-GGA	CACCCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTATTG TTTAGATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATA GAAACAGTGTATGCAGCCTATTTGCCCAAAAACAC	3080
	GTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGGCTT TTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATAAAA AGAAAGCAACCAGTTCAAACTGTCCTGAGGGGTG	3081
	TCTGGTAGAATCAACTT	3082

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAGTTGATTCTACCAGA	3083
Non-polypoid colorectal cancer Ser269Term TCA-TGA	CCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTATTGTTTA GATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATAGAAA CAGTGTATGCAGCCTATTTGCCCAAAAACACACA	3084
	TGTGTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGG CTTTTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATA AAAAGAAAGCAACCAGTTCAAACTGTCCTGAGGG	3085
	GGTAGAATCAACTTCCT	3086
	AGGAAGTTGATTCTACC	3087
Non-polypoid colorectal cancer Glu297Term GAA-TAA	CTTTTCTCCCCCTCCCACTATCTAAGGTAATTGTTCTCTCTTA TTTTCTGACAGTTTAGAAATCAGTCCCCAGAATGTGGATGTT AATGTGCACCCCAAAAGCATGAAGTTCACTTCC	3088
	GGAAGTGAACCTCATGCTTTGTGGGGTGCACATTAACATCCA CATTCTGGGGACTGATTTCTAACTGTCAGGAAAATAAGAGAG ACAATTACCTTAGATAGTGGGAGGGGGAGAAAAAG	3089
	ACAGTTTAGAAATCAGT	3090
	ACTGATTTCTAACTGT	3091
Non-polypoid colorectal cancer Gln301Term CAG-TAG	CTCCCACTATCTAAGGTAATTGTTCTCTCTTATTTCTGACAG TTTAGAAATCAGTCCCCAGAATGTGGATGTTAATGTGCACCCC ACAAAGCATGAAGTTCACTTCCTGCACGAGGAGA	3092
	TCTCCTCGTGCAGGAAGTGAACCTCATGCTTTGTGGGGTGCA CATTACATCCACATTCTGGGGACTGATTTCTAACTGTCAGG AAAATAAGAGAGAACAAATTACCTTAGATAGTGGGAG	3093
	TCAGTCCCCAGAATGTG	3094
	CACATTCTGGGGACTGA	3095
Non-polypoid colorectal cancer Val326Ala GTG-GCG	ATGTGCACCCCAAAAGCATGAAGTTCACTTCCTGCACGAGG AGAGCATCCTGGAGCGGGTGCAGCAGCACATCGAGAGCAAG CTCCTGGGCTCCAATTCCTCCAGGATGTACTTCACCCA	3096
	TGGGTGAAGTACATCCTGGAGGAATTGGAGCCCAGGAGCTT GCTCTCGATGTGCTGCTGCACCCGCTCCAGGATGCTCTCCT CGTGCAGGAAGTGAACCTCATGCTTTGTGGGGTGCACAT	3097
	GGAGCGGGTGCAGCAGC	3098
	GCTGCTGCACCCGCTCC	3099
Non-polypoid colorectal cancer His329Pro CAC-CCC	CCACAAAGCATGAAGTTCACTTCCTGCACGAGGAGAGCATCC TGGAGCGGGTGCAGCAGCACATCGAGAGCAAGCTCCTGGGC TCCAATTCCTCCAGGATGTACTTCACCCAGGTCAGGGC	3100
	GCCCTGACCTGGGTGAAGTACATCCTGGAGGAATTGGAGCC CAGGAGCTTGCTCTCGATGTGCTGCTGCACCCGCTCCAGGA TGCTCTCCTCGTGCAGGAAGTGAACCTCATGCTTTGTGG	3101
	GCAGCAGCACATCGAGA	3102
	TCTCGATGTGCTGCTGC	3103

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Non-polyposis colorectal cancer Val384Asp GTT-GAT	CAAGTCTGACCTCGTCTTCTACTTCTGGAAGTAGTGATAAGGT CTATGCCCACCAGATGGTTCGTACAGATTCCCGGGAACAGAA GCTTGATGCATTTCTGCAGCCTCTGAGCAAACCCCT	3104
	AGGGGTTTGCTCAGAGGCTGCAGAAATGCATCAAGCTTCTGT TCCCGGGAATCTGTACGAACCATCTGGTGGGCATAGACCTTA TCACTACTTCCAGAAGTAGAAGACGAGGTCAGACTTG	3105
	CCAGATGGTTCGTACAG	3106
	CTGTACGAACCATCTGG	3107
Non-polyposis colorectal cancer Ala441Thr GCT-ACT	AGTGGCAGGGCTAGGCAGCAAGATGAGGAGATGCTTGAAC CCCAGCCCCTGCTGAAGTGGCTGCCAAAATCAGAGCTTGGA GGGGGATACAACAAAGGGGACTTCAGAAATGTCAGAGA	3108
	TCTCTGACATTTCTGAAGTCCCCTTTGTTGTATCCCCCTCCAA GCTCTGATTTTTGGCAGCCACTTCAGCAGGGGCTGGGAGTTC AAGCATCTCCTCATCTTGCTGCCTAGCCCTGCCACT	3109
	CTGAAGTGGCTGCCAA	3110
	TTTGGCAGCCACTTCAG	3111
Non-polyposis colorectal cancer Arg487Term CGA-TGA	CTTCATTGCAGAAAGAGACATCGGGAAGATTCTGATGTGGAA ATGGTGGAAGATGATTCCCGAAAGGAAATGACTGCAGCTTGT ACCCCCCGGAGAAGGATCATTAACCTCACTAGTGTTT	3112
	AAACACTAGTGAGGTTAATGATCCTTCTCCGGGGGGTACAAG CTGCAGTCATTTCTTTTCGGGAATCATCTTCCACCATTTCAC ATCAGAATCTTCCCGATGTCTCTTTCTGCAATGAAG	3113
	ATGATTCCCGAAAGGAA	3114
	TTCCTTTTCGGGAATCAT	3115
Non-polyposis colorectal cancer Ala492Thr GCA-ACA	AGACATCGGGAAGATTCTGATGTGGAAATGGTGGAAAGATGAT TCCCGAAAGGAAATGACTGCAGCTTGTACCCCCCGGAGAAG GATCATTAACCTCACTAGTGTTTTGAGTCTCCAGGAAG	3116
	CTTCCTGGAGACTCAAACACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTGCAGTCATTTCTTTTCGGGAATCATC TTCCACCATTTCACATCAGAATCTTCCCGATGTCT	3117
	AAATGACTGCAGCTTGT	3118
	ACAAGCTGCAGTCATTT	3119
Non-polyposis colorectal cancer Val506Ala GTT-GCT	CCCGAAAGGAAATGACTGCAGCTTGTACCCCCCGGAGAAGG ATCATTAACCTCACTAGTGTTTTGAGTCTCCAGGAAGAAATTA ATGAGCAGGGACATGAGGGTACGTAAACGCTGTGGCC	3120
	GGCCACAGCGTTTACGTACCCTCATGTCCCTGCTCATTAATTT CTTCCTGGAGACTCAAACACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTGCAGTCATTTCTTTTCGGG	3121
	CACTAGTGTTTTGAGTC	3122
	GACTCAAACACTAGTG	3123
Non-polyposis colorectal cancer Gln542Leu CAG-CTG	GGGAGATGTTGCATAACCACTCCTTCGTGGGCTGTGTGAATC CTCAGTGGGCCTTGGCACAGCATCAAACCAAGTTATACCTTC TCAACACCACCAAGCTTAGGTAAATCAGCTGAGTGTG	3124

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACACTCAGCTGATTACCTAAGCTTGGTGGTGTGAGAAGG TATAACTTGGTTTGATGCTGTGCCAAGGCCCACTGAGGATTC ACACAGCCACGAAGGAGTGGTTATGCAACATCTCCC	3125
	CTTGGCACAGCATCAA	3126
	TTTGATGCTGTGCCAAG	3127
Non-polypoid colorectal cancer Leu549Pro CTT-CCT	CCTTCGTGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAG CATCAAACCAAGTTATACCTTCTCAACACCACCAAGCTTAGGT AAATCAGCTGAGTGTGTGAACAAGCAGAGCTACTACA	3128
	TGTAGTAGCTCTGCTTGTTCACACACTCAGCTGATTACCTAA GCTTGGTGGTGTGAGAAGGTATAACTTGGTTTGATGCTGTG CCAAGGCCCACTGAGGATTCACACAGCCACGAAGG	3129
	GTTATACCTTCTCAACA	3130
	TGTTGAGAAGGTATAAC	3131
Non-polypoid colorectal cancer Asn551Thr AAC-ACC	TGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAGCATCAA CCAAGTTATACCTTCTCAACACCACCAAGCTTAGGTAAATCAG CTGAGTGTGTGAACAAGCAGAGCTACTACAACAATG	3132
	CATTGTTGTAGTAGCTCTGCTTGTTCACACACTCAGCTGATT ACCTAAGCTTGGTGGTGTGAGAAGGTATAACTTGGTTTGATG CTGTGCCAAGGCCCACTGAGGATTCACACAGCCCA	3133
	CCTTCTCAACACCACCA	3134
	TGGTGGTGTGAGAAGG	3135
Non-polypoid colorectal cancer Gln562Term CAG-TAG	ATGAATTCAGCTTTTCCTTAAAGTCACTTCATTTTATTTTCAG TGAAGAAGTGTCTACAGATACTCATTTATGATTTTGCCAATT TTGGTGTCTCAGGTTATCGGTAAGTTTAGATC	3136
	GATCTAAACTTACCGATAACCTGAGAACACCAAAATTGGCAA ATCATAAATGAGTATCTGGTAGAACAGTTCTTCACTGAAAATA AAAATGAAGTGACTTTAAGGAAAAGCTGAATTCAT	3137
	TGTTCTACAGATACTC	3138
	GAGTATCTGGTAGAACA	3139
Non-polypoid colorectal cancer Ile565Phe ATT-TTT	GCTTTTCCTTAAAGTCACTTCATTTTATTTTCAGTGAAGAACT GTTCTACAGATACTCATTTATGATTTTGCCAATTTTGGTGTTC TCAGGTTATCGGTAAGTTTAGATCCTTTTCACT	3140
	AGTGAAAAGGATCTAACTTACCGATAACCTGAGAACACCAAA ATTGGCAAATCATAAATGAGTATCTGGTAGAACAGTTCTTCA CTGAAAATAAAAATGAAGTGACTTTAAGGAAAAGC	3141
	AGATACTCATTTATGAT	3142
	ATCATAAATGAGTATCT	3143
Non-polypoid colorectal cancer Leu574Pro CTC-CCC	TTTTCAGTGAAGAACTGTTCTACAGATACTCATTTATGATTT GCCAATTTTGGTGTTCCTCAGGTTATCGGTAAGTTTAGATCCTT TTCACCTCTGAAATTTCAACTGATCGTTTCTGAA	3144
	TTCAGAAACGATCAGTTGAAATTTGAGAAGTGAAAAGGATCTA AACTTACCGATAACCTGAGAACACCAAAATTGGCAAATCATA AATGAGTATCTGGTAGAACAGTTCTTCACTGAAAA	3145
	TGGTGTCTCAGGTTAT	3146

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAACCTGAGAACACCA	3147
Non-polypoidis colorectal cancer Leu582Val CTC-GTC	TGGATGCTCCGTTAAAGCTTGCTCCTTCATGTTCTTGCTTCTT CCTAGGAGCCAGCACCGCTCTTTGACCTTGCCATGCTTGCCT TAGATAGTCCAGAGAGTGGCTGGACAGAGGAAGATG	3148
	CATCTTCCTCTGTCCAGCCACTCTCTGGACTATCTAAGGCAA GCATGGCAAGGTCAAAGAGCGGTGCTGGCTCCTAGGAAGAA GCAAGAACATGAAGGAGCAAGCTTTAACGGAGCATCCA	3149
	CAGCACCGCTCTTTGAC	3150
	GTCAAAGAGCGGTGCTG	3151
Non-polypoidis colorectal cancer Leu607His CTT-CAT	TGCTTGCCTTAGATAGTCCAGAGAGTGGCTGGACAGAGGAAG ATGGTCCCAAAGAAGGACTTGCTGAATACATTGTTGAGTTTCT GAAGAAGAAGGCTGAGATGCTTGCAGACTATTTCTC	3152
	GAGAAATAGTCTGCAAGCATCTCAGCCTTCTTCTTCAGAACT CAACAATGTATTCAGCAAGTCCTTCTTTGGGACCATCTTCCTC TGTCAGCCACTCTCTGGACTATCTAAGGCAAGCA	3153
	AGAAGGACTTGCTGAAT	3154
	ATTCAGCAAGTCCTTCT	3155
Non-polypoidis colorectal cancer Lys618Term AAG-TAG	ACAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATT GTTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTAT TTCTCTTTGGAAATTGATGAGGTGTGACAGCCATTCT	3156
	AGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGTC TGCAAGCATCTCAGCCTTCTTCTTCAGAACTCAACAATGTAT TCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTGT	3157
	TGAAGAAGAAGGCTGAG	3158
	CTCAGCCTTCTTCTTCA	3159
Non-polypoidis colorectal cancer Lys618Thr AAG-ACG	CAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATTG TTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTATTT CTCTTTGGAAATTGATGAGGTGTGACAGCCATTCTT	3160
	AAGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGT CTGCAAGCATCTCAGCCTTCTTCTTCAGAACTCAACAATGTA TTCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTG	3161
	GAAGAAGAAGGCTGAGA	3162
	TCTCAGCCTTCTTCTTC	3163
Non-polypoidis colorectal cancer Arg659Leu CGA-CTA	TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCGGTACATGCATGTGTGC	3164
	GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTA	3165
	CATTCTTCGACTAGCCA	3166
	TGGCTAGTCGAAGAATG	3167

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polypoid colorectal cancer Arg659Pro CGA-CCA	TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCGGTACATGCATGTGTGC	3168
	GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTA	3169
	CATTCTTCGACTAGCCA	3170
	TGGCTAGTGAAGAATG	3171
Non-polypoid colorectal cancer Arg659Term CGA-TGA	TTACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGA CTGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATC AAGCAGATACTAAGCATTTCGGTACATGCATGTGTG	3172
	CACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCACT GACCTCAGTGGCTAGTGAAGAATGAAGATAGGCAGTCCCTC CAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTAA	3173
	TCATTCTTCGACTAGCC	3174
	GGCTAGTGAAGAATGA	3175
Non-polypoid colorectal cancer Ala681Thr GCT-ACT	TTGGACCAGGTGAATTGGGACGAAGAAAAGGAATGTTTTGAA AGCCTCAGTAAAGAATGCGCTATGTTCTATTCCATCCGGAAG CAGTACATATCTGAGGAGTCGACCCTCTCAGGCCAGC	3176
	GCTGGCCTGAGAGGGTCGACTCCTCAGATATGTACTGCTTCC GGATGGAATAGAACATAGCGCATTCTTACTGAGGCTTTCAA ACATTCTTTCTTCGTCCCAATTCACCTGGTCCAA	3177
	AAGAATGCGCTATGTTT	3178
	GAACATAGCGCATTCTT	3179
Non-polypoid colorectal cancer Trp712Term TGG-TAG	AGGCTTATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGG CTCCATTCCAACTCCTGGAAGTGGACTGTGGAACACATTGT CTATAAAGCCTTGCCTCACACATTCTGCCTCCTAA	3180
	TAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATG TGTTCCACAGTCCACTTCCAGGAGTTTGGAAATGGAGCCAGGC ACTTCACTCTGGAAACACATTAGATGTCATAAGCCT	3181
	AACTCCTGGAAGTGG	3182
	TCCACTTCCAGGAGTTT	3183
Non-polypoid colorectal cancer Trp714Term TGG-TAG	ATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCAT TCCAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAA GCCTTGCCTCACACATTCTGCCTCCTAAACATT	3184
	AAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAG ACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAAATGGAG CCAGGCACTTCACTCTGGAAACACATTAGATGTCAT	3185
	CTGGAAGTGGACTGTGG	3186
	CCACAGTCCACTTCCAG	3187
Non-polypoid colorectal cancer Trp714Term TGG-TGA	TGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATT CCAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAA GCCTTGCCTCACACATTCTGCCTCCTAAACATTTC	3188

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATA GACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAAATGGA GCCAGGCACTTCACTCTGGAAAACACATTAGATGTCA	3189
	TGGAAGTGGACTGTGGA	3190
	TCCACAGTCCACTTCCA	3191
Non-polyposis colorectal cancer Val716Met GTG-ATG	ATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAA ACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAAGCCTT GCGCTCACACATTCTGCCTCCTAAACATTTACAG	3192
	CTGTGAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTT TATAGACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAAAT GGAGCCAGGCACTTCACTCTGGAAAACACATTAGAT	3193
	AGTGGACTGTGGAACAC	3194
	GTGTTCCACAGTCCACT	3195
Non-polyposis colorectal cancer Tyr721Term TAT-TAA	GAGTGAAGTGCCTGGCTCCATTCCAACTCCTGGAAGTGGAC TGTGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTG CCTCCTAAACATTTACAGAAAGATGGAAATATCCTG	3196
	CAGGATATTTCCATCTTCTGTGAAATGTTTAGGAGGCAGAATG TGTGAGCGCAAGGCTTTATAGACAATGTGTTCCACAGTCCAC TTCCAGGAGTTTGGAAATGGAGCCAGGCACTTCACTC	3197
	ATTGTCTATAAAGCCTT	3198
	AAGGCTTTATAGACAAT	3199
Non-polyposis colorectal cancer Lys751Arg AAA-AGA	CTAAACATTTACAGAAAGATGGAAATATCCTGCAGCTTGCTAA CCTGCCTGATCTATACAAAGTCTTTGAGAGGTGTTAAATATGG TTATTTATGCACTGTGGGATGTGTTCTTCTTTCTC	3200
	GAGAAAGAAGAACACATCCCACAGTGCATAAATAACCATATTT AACACCTCTCAAAGACTTTGTATAGATCAGGCAGGTTAGCAAG CTGCAGGATATTTCCATCTTCTGTGAAATGTTTAG	3201
	TCTATACAAAGTCTTTG	3202
	CAAAGACTTTGTATAGA	3203
Non-polyposis colorectal cancer Arg755Trp AGG-TGG	ACAGAAGATGGAAATATCCTGCAGCTTGCTAACCTGCCTGAT CTATACAAAGTCTTTGAGAGGTGTTAAATATGGTTATTTATGCA CTGTGGGATGTGTTCTTCTTTCTCTGTATTCCGAT	3204
	ATCGGAATACAGAGAAAGAAGAACACATCCCACAGTGCATAA ATAACCATATTTAACACCTCTCAAAGACTTTGTATAGATCAGG CAGGTTAGCAAGCTGCAGGATATTTCCATCTTCTGT	3205
	TCTTTGAGAGGTGTTAA	3206
	TTAACACCTCTCAAAGA	3207

EXAMPLE 18**Human mismatch repair - MSH2**

The human MSH2 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH2 gene have been identified in a variety of cancers, including, for

example, ovarian tumors, colorectal cancer, endometrial cancer, uterine cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH2 oligonucleotides of the invention.

Table 25
MSH2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Gln252Term CAG-TAG	TTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGA AAGGCAAAAAGGGAGAGCAGATGAATAGTGCTGTATTGCCAG AAATGGAGAATCAGGTACATGGATTATAAATGTGAA	3208
	TTCACATTTATAATCCATGTACCTGATTCTCCATTTCTGGCAAT ACAGCACTATTCATCTGCTCTCCCTTTTTGCCTTTCAACAACC GGTTGAGGTCCTGATAAATGTCTTTTGTGGAAAA	3209
	AGGGAGAGCAGATGAAT	3210
	ATTCATCTGCTCTCCCT	3211
Non polyposis colorectal cancer Gln288Term CAG-TAG	TCATCACTGTCTGCGGTAATCAAGTTTTAGAACTCTTATCAG ATGATTCCAACCTTTGGACAGTTTGAAGTACTACTTTTGAAGT CAGCCAGTATATGAAATTGGATATTGCAGCAGTCA	3212
	TGACTGCTGCAATATCCAATTCATATACTGGCTGAAGTCAA AGTAGTCAGTTCAAAGTGTCCAAAGTTGGAATCATCTGATAAG AGTTCTAAAACTTGATTACCGCAGACAGTGATGA	3213
	ACTTTGGACAGTTTGAA	3214
	TTCAAAGTGTCCAAAGT	3215
Non polyposis colorectal cancer Ala305Thr GCA-ACA	AACTTTGGACAGTTTGAAGTACTACTTTTGAAGTTCAGCCAGT ATATGAAATTGGATATTGCAGCAGTCAGAGCCCTTAACCTTTT TCAGGTAAAAAAGG	3216
	CCTTTTTTTTTTTTTTTTTTTTTTTTACCTGAAAAGGTTAAG GGCTCTGACTGCTGCAATATCCAATTCATATACTGGCTGAAG TCAAAGTAGTCAGTTCAAAGTGTCCAAAGTT	3217
	TGGATATTGCAGCAGTC	3218
	GACTGCTGCAATATCCA	3219
Non polyposis colorectal cancer Gly322Asp GGC-GAC	AGCTTGCCATTCTTTCTATTTTATTTTTGTTTACTAGGGTTCT GTTGAAGATACCACTGGCTCTCAGTCTCTGGCTGCCTTGCTG AATAAGTGTAACCCCTCAAGGACAAAGACTTGT	3220
	ACAAGTCTTTGTCCTTGAGGGGTTTTACACTTATTCAGCAAGG CAGCCAGAGACTGAGAGCCAGTGGTATCTTCAACAGAACCCT AGTAAACAAAAATAAAATAGAAAGAAATGGCAAGCT	3221
	TACCACTGGCTCTCAGT	3222
	ACTGAGAGCCAGTGGTA	3223
Non polyposis colorectal cancer Ser323Cys TCT-TGT	TTGCCATTCTTTCTATTTTATTTTTGTTTACTAGGGTTCTGTTG AAGATACCACTGGCTCTCAGTCTCTGGCTGCCTTGCTGAATA AGTGTAACCCCTCAAGGACAAAGACTTGTTAA	3224
	TTAACAAGTCTTTGTCCTTGAGGGGTTTTACACTTATTCAGCA AGGCAGCCAGAGACTGAGAGCCAGTGGTATCTTCAACAGAAC CCTAGTAACAAAAATAAAATAGAAAGAAATGGCAA	3225

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACTGGCTCTCAGTCTC	3226
	GAGACTGAGAGCCAGTG	3227
Non polyposis colorectal cancer Arg383Term CGA-TGA	GTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTA CAAGAAGATTTACTTCGTGATTCCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAG	3228
	CTTGTAAGTTTGCTGCTTGTCTTTGAACTTCTTGGCAAGTCG GTTAAGATCTGGGAATCGACGAAGTAAATCTTCTTGTAAGTC TGCCTCAATTCTGCATCTTCTACAAAAGCTTCCAC	3229
	TACTTCGTGATTCCCA	3230
	TGGGAATCGACGAAGTA	3231
Non polyposis colorectal cancer Gln397Term CAA-TAA	CAAGAAGATTTACTTCGTGATTCCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAGATTGTTA CCGACTCTATCAGGGTATAAATCAACTACCTAATG	3232
	CATTAGGTAGTTGATTTATACCCTGATAGAGTCGGTAACAATC TTGTAAGTTTGCTGCTTGTCTTTGAACTTCTTGGCAAGTCGG TTAAGATCTGGGAATCGACGAAGTAAATCTTCTTG	3233
	TTCAAAGACAAGCAGCA	3234
	TGCTGCTTGTCTTTGAA	3235
Non polyposis colorectal cancer Arg406Term CGA-TGA	GATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCA AACTTACAAGATTGTTACCGACTCTATCAGGGTATAAATCAAC TACCTAATGTTATACAGGCTCTGGAAAAACATGAAG	3236
	CTTCATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTT ATACCCTGATAGAGTCGGTAACAATCTTGTAAGTTTGCTGCTT GTCTTTGAACTTCTTGGCAAGTCGGTTAAGATC	3237
	ATTGTTACCGACTCTAT	3238
	ATAGAGTCGGTAACAAT	3239
Non polyposis colorectal cancer Gln419Term CAG-TAG	GCAAACCTTACAAGATTGTTACCGACTCTATCAGGGTATAAATC AACTACCTAATGTTATACAGGCTCTGGAAAAACATGAAGGTAA CAAGTGATTTTGTGTTTTTGTGTTTCCCTTCAACTCA	3240
	TGAGTTGAAGGAAAAACAAAAAACAATCACTTGTTACCTTC ATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTTATAC CCTGATAGAGTCGGTAACAATCTTGTAAGTTTGC	3241
	ATGTTATACAGGCTCTG	3242
	CAGAGCCTGTATAACAT	3243
Non polyposis colorectal cancer Gln429Term CAG-TAG	TATTCTGTAAAATGAGATCTTTTATTTGTTTGTGTTTACTACTTT CTTTTAGGAAAACACCAGAAATTATTGTTGGCAGTTTTTGTGA CTCCTCTTACTGATCTTCGTTCTGACTTCTCCA	3244
	TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAGTCACAAAAA CTGCCAACAATAATTTCTGGTGTTTTCCTAAAAGAAAGTAGTA AAACAAACAAATAAAAAGATCTCATTTACAGAATA	3245
	GAAACACCAGAAATTA	3246
	TAATTTCTGGTGTTTC	3247

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Leu458Term TTA-TGA	CTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTCAGGA AATGATAGAAACAACCTTTAGATATGGATCAGGTATGCAATATA CTTTTTAATTTAAGCAGTAGTTATTTTTAAAAAGC	3248
	GCTTTTTAAAAATAACTACTGCTTAAATTTAAAAAGTATATTGCA TACCTGATCCATATCTAAAGTTGTTTCTATCATTTCCTGAAACT TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAG	3249
	AACAACCTTTAGATATGG	3250
	CCATATCTAAAGTTGTT	3251
	TTTCTTCTTGATTATCAAGGCTTGGACCCTGGCAAACAGATTA AACTGGATTCCAGTGCACAGTTTGGATATTACTTTCTGTGTAAAC CTGTAAGGAAGAAAAAGTCCTTCGTAACAATAAAA	3252
Non polyposis colorectal cancer Gln518Term CAG-TAG	TTTTATTGTTACGAAGGACTTTTTCTTCCTTACAGGTTACACGA AAGTAATATCCAACTGTGCACTGGAATCCAGTTTAATCTGTT TGCCAGGGTCCAAGCCTTGATAATCAAGAAGAAA	3253
	CCAGTGCACAGTTTGGG	3254
	TCCAACTGTGCACTGG	3255
	GCTTGGACCCTGGCAAACAGATTAACTGGATTCCAGTGCAC AGTTTGGATATTACTTTCTGTGTAAACCTGTAAGGAAGAAAAAGT CCTTCGTAACAATAAAAACTTTAGTACTGTAGATAT	3256
	ATATCTACAGTACTAAAGTTTTATTGTTACGAAGGACTTTTTCT TTCCTTACAGGTTACAGGAAAGTAATATCCAACTGTGCACTG GAATCCAGTTTAATCTGTTTGCCAGGGTCCAAGC	3257
Non polyposis colorectal cancer Arg524Pro CGT-CCT	TTACTTTCTGTGAACCT	3258
	AGGTTACACGAAAGTAA	3259
	TTAATATTTTAAATAAACTGTTATTTCTGATTTGCAGCAAATTGA CTTCTTTAAATGAAGAGTATACCAAAAATAAAACAGAATATGAA GAAGCCCAGGATGCCATTGTTAAAGAAATTGT	3260
	ACAATTTCTTTAACAATGGCATCCTGGGCTTCTTCATATTCTGT TTTATTTTTGGTATACTCTTCATTTAAAGAAGTCAATTTGCTGC AAATCGAAATAACAGTTTATTAAAAATATTAA	3261
	AAATGAAGAGTATACCA	3262
Glioma Glu580Term GAA-TAA	TGGTATACTCTTCATT	3263
	AATGAAGAGTATACCAAAAATAAAACAGAATATGAAGAAGCCC AGGATGCCATTGTTAAAGAAATTGTCAATATTTCTTCAGGTAAA CTTAATAGAACTAATAATGTTCTGAATGTCACCT	3264
	AGGTGACATTCAGAACATTATTAGTTCTATTAAGTTTACCTGAA GAAATATTGACAATTTCTTTAACAATGGCATCCTGGGCTTCTT CATATTCTGTTTTATTTTTGGTATACTCTTCATT	3265
	TTGTAAAGAAATTGTC	3266
	GACAATTTCTTTAACAA	3267
Non polyposis colorectal cancer Gln601Term CAG-TAG	TGTTTTATTTTTATACAGGCTATGTAGAACCAATGCAGACACT CAATGATGTGTTAGCTCAGCTAGATGCTGTTGTCAGCTTTGCT CACGTGTCAAATGGAGCACCTGTTCCATATGTAC	3268

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTACATATGGAACAGGTGCTCCATTTGACACGTGAGCAAAGC TGACAACAGCATCTAGCTGAGCTAACACATCATTGAGTGTCTG CATTGGTTCTACATAGCCTGTATAAAAATAAAAACA	3269
	TGTTAGCTCAGCTAGAT	3270
	ATCTAGCTGAGCTAACA	3271
Non polyposis colorectal cancer Tyr619Term TAT-TAG	AGCTCAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAAT GGAGCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAA GGACAAGGAAGAATTATATTAAGCATCCAGGCAT	3272
	ATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTCTCCA AAATGGCTGGTCGTACATATGGAACAGGTGCTCCATTTGACA CGTGAGCAAAGCTGACAACAGCATCTAGCTGAGCT	3273
	GTTCCATATGTACGACC	3274
	GGTCGTACATATGGAAC	3275
Non polyposis colorectal cancer Arg621Term CGA-TGA	CAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGA GCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGA CAAGGAAGAATTATATTAAGCATCCAGGCATGCTT	3276
	AAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTC TCCAAAATGGCTGGTCGTACATATGGAACAGGTGCTCCATTT GACACGTGAGCAAAGCTGACAACAGCATCTAGCTG	3277
	CATATGTACGACCAGCC	3278
	GGCTGGTCGTACATATG	3279
Non polyposis colorectal cancer Pro622Leu CCA-CTA	TAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGAGCAC CTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAAG GAAGAATTATATTAAGCATCCAGGCATGCTTGTGT	3280
	ACACAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTC CTTTCTCCAAAATGGCTGGTCGTACATATGGAACAGGTGCTC CATTTGACACGTGAGCAAAGCTGACAACAGCATCTA	3281
	TGTACGACCAGCCATTT	3282
	AAATGGCTGGTCGTACA	3283
Non polyposis colorectal cancer Ala636Pro GCA-CCA	CCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAA GGAAGAATTATATTAAGCATCCAGGCATGCTTGTGTTGAAG TTCAAGATGAAATTGCATTTATTCCTAATGACGTAT	3284
	ATACGTCATTAGGAATAAATGCAATTTATCTTGAACCTCAACA CAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTT CTCCAAAATGGCTGGTCGTACATATGGAACAGG	3285
	TATTAAGCATCCAGG	3286
	CCTGGATGCTTTTAATA	3287
Non polyposis colorectal cancer His639Arg CAT-CGT	ATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATTA TATTAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATGA AATTGCATTTATTCCTAATGACGTATACTTTGAAA	3288
	TTTTCAAAGTATACGTCATTAGGAATAAATGCAATTTATCTTG AACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTTC CTTGTCCTTTCTCCAAAATGGCTGGTCGTACAT	3289
	ATCCAGGCATGCTTGTG	3290

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CACAAGCATGCCTGGAT	3291
Non polyposis colorectal cancer His639Tyr CAT-TAT	TATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATT	3292
	ATATTAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATG	
	AAATTGCATTTATTCCTAATGACGTATACTTTGAAA	
	TTTCAAAGTATACGTCATTAGGAATAAATGCAATTTTCATCTTGA	3293
	ACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTTC	
	CTTGTCCTTTCTCCAAATGGCTGGTCGTACATA	
	CATCCAGGCATGCTTGT	3294
	ACAAGCATGCCTGGATG	3295
Non polyposis colorectal cancer Glu647Lys GAA-AAA	AAAGGACAAGGAAGAATTATATTAAGCATCCAGGCATGCTT	3296
	GTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTAATGACGT	
	ATACTTTGAAAAAGATAAACAGATGTTCCACATCA	
	TGATGTGGAACATCTGTTTATCTTTTCAAAGTATACGTCATTA	3297
	GGAATAAATGCAATTTTCATCTTGAACCTTCAACACAAGCATGCC	
	TGGATGCTTTTAATATAATTCTTCCTTGTCTTT	
	TTCAAGATGAAATTGCA	3298
	TGCAATTTTCATCTTGAA	3299
Non polyposis colorectal cancer Tyr656Term TAC-TAG	ATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTT	3300
	ATTCCTAATGACGTATACTTTGAAAAAGATAAACAGATGTTCCA	
	CATCATTACTGGTAAAAACCTGGTTTTTGGGCT	
	AGCCCCAAAACCAGGTTTTTTACCAGTAATGATGTGGAACATC	3301
	TGTTTATCTTTTCAAAGTATACGTCATTAGGAATAAATGCAAT	
	TTCATCTTGAACCTTCAACACAAGCATGCCTGGAT	
	GACGTATACTTTGAAA	3302
	TTTTCAAAGTATACGTC	3303
Non polyposis colorectal cancer Gly674Asp GGT-GAT	GAAAGAAGTTTAAATCTTGCTTTCTGATATAATTTGTTTTGTA	3304
	GGCCCCAATATGGGAGGTAAATCAACATATATTCGACAACT	
	GGGGTGATAGTACTCATGGCCCCAATTGGGTGTTT	
	AAACACCCAATTTGGGCCATGAGTACTATCACCCCAGTTTGTC	3305
	GAATATATGTTGATTACCTCCCATATTGGGGCCTACAAAACA	
	AATTATATCAGAAAGCAAGATTTTAACTTCTTTC	
	TATGGGAGGTAAATCAA	3306
	TTGATTTACCTCCATA	3307
Non polyposis colorectal cancer Arg680Term CGA-TGA	TTGCTTTCTGATATAATTTGTTTTGTAGGCCCAATATGGGAG	3308
	GTAATCAACATATATTCGACAACTGGGGTGATAGTACTCAT	
	GGCCCCAATTGGGTGTTTTGTGCCATGTGAGTCAG	
	CTGACTCACATGGCACAAAACACCCAATTTGGGCCATGAGTA	3309
	CTATACCCCAGTTTGTCGAATATATGTTGATTACCTCCCAT	
	ATTGGGGCCTACAAAACAATTATATCAGAAAGCAA	
	CATATATTCGACAACT	3310
	AGTTTGTGCAATATATG	3311

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Non polyposis colorectal cancer Gly692Arg GGG-CGG	ATGGGAGGTAATCAACATATATTCGACAACTGGGGTGATA GTA ^T CTCATGGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCA GCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGAG	3312
	CTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACT CACATGGCACAAAACACCCAAATTTGGGCCATGAGTACTATCA CCCCAGTTTGTCTGAATATATGTTGATTACCTCCCAT	3313
	CCCAAATTGGGTGTTTT	3314
	AAACACCCAAATTTGGG	3315
Non polyposis colorectal cancer Cys697Arg TGT-CGT	ACATATATTCGACAACTGGGGTGATAGTACTCATGGCCCAA TTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCCATTG TGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACA	3316
	TGTCACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATGG ACACTTCTGCTGACTCACATGGCACAAAACACCCAAATTTGGG CCATGAGTACTATCACCCAGTTTGTCTGAATATATGT	3317
	TTGTGCCATGTGAGTCA	3318
	TGACTCACATGGCACAA	3319
Non polyposis colorectal cancer Cys697Phe TGT-TTT	CATATATTCGACAACTGGGGTGATAGTACTCATGGCCCAAAT TGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCCATTGT GGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAG	3320
	CTGTACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATG GACACTTCTGCTGACTCACATGGCACAAAACACCCAAATTTGG GCCATGAGTACTATCACCCAGTTTGTCTGAATATATG	3321
	TGTGCCATGTGAGTCAG	3322
	CTGACTCACATGGCACAA	3323
Non polyposis colorectal cancer Gln718Term CAA-TAA	GAGTCAGCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGA GTAGGGGCTGGTGACAGTCAATTGAAAGGAGTCTCCACGTTCT ATGGCTGAAATGTTGGAACTGCTTCTATCCTCAGGT	3324
	ACCTGAGGATAGAAGCAGTTTCCAACATTTAGCCATGAACG TGGAGACTCCTTTCAATTGACTGTCACCAGCCCCTACTCGGG CTAAGATGCAGTCCACAATGGACACTTCTGCTGACTC	3325
	GTGACAGTCAATTGAAA	3326
	TTTCAATTGACTGTCAC	3327
Non polyposis colorectal cancer Leu811Term TTA-TGA	CCAATCAGATACCAACTGTTAATAATCTACATGTCACAGCACT CACCCTGAAGAGACCTTA ^T ACTATGCTTTATCAGGTGAAGAAA GGTATGTACTATTGGAGTACTCTAAATTCAGAACT	3328
	AGTTCTGAATTTAGAGTACTCCAATAGTACATACCTTTCTTCAC CTGATAAAGCATAGTTAAGGTCTCTTCAGTGGTGAGTGCTGT GACATGTAGATTATTAACAGTTGGTATCTGATTGG	3329
	AGAGACCTTA ^T ACTATGC	3330
	GCATAGTTAAGGTCTCT	3331
Non polyposis colorectal cancer Ala834Thr GCT-ACT	TTCCCCAAATTTCTTATAGGTGTCTGTGATCAAAGTTTTGGGA TTCATGTTGCAGAGCTTGCTAATTTCCCTAAGCATGTAATAGA GTGTGCTAAACAGAAAGCCCTGGAACCTTGAGGAGT	3332

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTCCTCAAGTTCCAGGGCTTTCTGTTTAGCACACTCTATTAC ATGCTTAGGGAAATTAGCAAGCTCTGCAACATGAATCCCAAAA CTTTGATCACAGACACCTATAAGAAATTTGGGGAA	3333
	CAGAGCTTGCTAATTC	3334
	GAAATTAGCAAGCTCTG	3335
	ATAGAGTGTGCTAAACAGAAAGCCCTGGAAGTTGAGGAGTTT CAGTATATTGGAGAATCGCAAGGATATGATATCATGGAACCAG CAGCAAAGAAGTGCTATCTGGAAAGAGAGGTTTGTC	3336
Non polyposis colorectal cancer Gln861Term CAA-TAA	GACAAACCTCTCTTTCCAGATAGCACTTCTTTGCTGCTGGTTC CATGATATCATATCCTTGCGATTCTCCAATATACTGAACTCCT CAAGTTCCAGGGCTTTCTGTTTAGCACACTCTAT	3337
	GAGAATCGCAAGGATAT	3338
	ATATCCTTGCGATTCTC	3339
	AGGAGTTCCTGTCCAAGGTGAAACAAATGCCCTTTACTGAAAT GTCAGAAGAAAACATCACAATAAAGTTAAACAGCTAAAAGCT GAAGTAATAGCAAAGAATAATAGCTTTGTAAATGA	3340
Non polyposis colorectal cancer Thr905Arg ACA-AGA	TCATTTACAAAGCTATTATTCTTTGCTATTACTTCAGCTTTTAG CTGTTTAACTTTATTGTGATGTTTTCTTCTGACATTTACGTAA AGGGCATTGTTCACCTTGGACAGGAACTCCT	3341
	AAACATCACAATAAAGT	3342
	ACTTTATTGTGATGTTT	3343

EXAMPLE 19

Human mismatch repair - MSH6

The human MSH6 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH6 gene have been identified in a variety of cancers, including particularly hereditary nonpolyposis colorectal cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH6 oligonucleotides of the invention.

Table 26

MSH6 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Ser144Ile AGC-ATC	GGAAATCAGTCCGTGTTTCATGTACAGTTTTTTGATGACAGCCC AACAAGGGGCTGGGTAGCAAAAGGCTTTTAAAGCCATATAC AGGTAAGAGTCACTACTGCCATGTGTGTGTGTTTGT	3344

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ACAAACACACACACATGGCAGTAGTGACTCTTACCTGTATATG GCTTTAAAAGCCTTTTGCTAACCCAGCCCCTTGTTGGGCTGT CATCAAAAAGCTGTACATGAACACGGACTGATTTCC	3345
	CTGGGTTAGCAAAGGC	3346
	GCCTTTTGCTAACCCAG	3347
Endometrial cancer Ser156Term TCA-TGA	CGTGAGCCTCTGCACCCGGCCCTTATTGTTTATAAATACATTT CTTTCTAGGTTCAAATCAAAGGAAGCCCAGAAGGGAGGTCA TTTTACAGTGCAAAGCCTGAAATACTGAGAGCAAT	3348
	ATTGCTCTCAGTATTTGAGGCTTTGCACTGTAAAATGACCTC CCTTCTGGGCTTCCTTTGATTTTGAACCTAGAAAGAAATGTAT TTATAACAATAAGGGCCGGGTGCAGAGGCTCACG	3349
	TTCAAATCAAAGGAAG	3350
	CTTCCTTTGATTTTGAA	3351
Early onset colorectal cancer Tyr214Term TAC-TAG	TTCAAATTTTGATTTGTTTTAAATACTCTTCCTTGCCTGGC AGGTAGGCACAACCTACGTAACAGATAAGAGTGAAGAAGATA ATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAG	3352
	CTTAGGCTGTACTTCCTCTTCACTCTCAATTCATTATCTTCTT CACTCTTATCTGTTACGTAAGTTGTGCCTACCTGCCAGGCAA GGAAAGAGTATTTAAAACAAATCAAATTTGGAA	3353
	ACAACCTACGTAACAGA	3354
	TCTGTTACGTAAGTTGT	3355
Endometrial cancer Arg248Term CGA-TGA	GAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGT AGCCGCCAAATAAAAAACGAAGGGTCATATCAGATTCTGAG AGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAG	3356
	CTGGCTTAAATTCCACATCAGAGCCACCAATGTCACTCTCAGA ATCTGATATGACCCTTCGTTTTTTTATTTGGCGGCTACTTCGC CTAGATCCTTGTGTCTTAGGCTGTACTTCCTCTTC	3357
	TAAAAAACGAAGGGTC	3358
	GACCCTTCGTTTTTTTA	3359
Colorectal cancer Ser285Ile AGT-ATT	TTAAGCCAGACACTAAGGAGGAAGGAAGCAGTGATGAAATAA GCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGC CCTGTCAAAGTTGCTCGAAAGCGGAAGAGAATGGTGAC	3360
	GTCACCATTCTCTCCGCTTTCGAGCAACTTTGACAGGGCTG TTCAGGCCTTCACTCTCACTATCCCCCACTCCACTGCTTATTT CATCACTGCTTCCTTCCTCCTTAGTGTCTGGCTTAA	3361
	GGGGGATAGTGAGAGTG	3362
	CACTCTCACTATCCCCC	3363
Colorectal cancer Gly566Arg GGA-AGA	GAGGAAGATTCTTC,GGCCATACTCGTGCAATATGGTGTGTGC TTTGTTGATACTTCACTGGGAAAGTTTTTCATAGGTCAGTTTTC AGATGATCGCCATTGTTGAGATTTAGGACTCTAG	3364

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTAGAGTCCTAAATCTCGAACAATGGCGATCATCTGAAACTG ACCTATGAAAACTTTCCAGTGAAGTATCAACAAAGCACACA CCATATGCACGAGTATGGCCAGAAGAATCTTCCTC CTTCACTGGGAAAGTTT	3365
	AAACTTTCCAGTGAAG	3366
		3367
		3368
Non-polypoid colorectal cancer Gln698Glu CAG-GAG	GAATTGGCCCTCTCTGCTCTAGGTGGTTGTGTCTTCTACCTC AAAAATGCCTTATTGATCAGGAGCTTTTATCAATGGCTAATTT TGAAGAATATATTCCCTTGGATTCTGACACAGTCA	3369
	TGACTGTGTCAGAATCCAAGGGAATATATTCTTCAAATTAGC CATTGATAAAAGCTCCTGATCAATAAGGCATTTTTTGTAGGTAG AAGACACAACCACCTAGAGCAGAGAGGGCCAATTC	3370
	TTATTGATCAGGAGCTT	3371
	AAGCTCCTGATCAATAA	3372
Endometrial cancer Gln731Term CAA-TAA	CCCTTGGATTCTGACACAGTCAGCACTACAAGATCTGGTGCT ATCTTCACCAAAGCCTATCAACGAATGGTGCTAGATGCAGTG ACATTAACAACCTTGGAGATTTTTCTGAATGGAACAA	3373
	TTGTTCCATTGAGAAAAATCTCCAAGTTGTTAATGTCACTGCA TCTAGCACCATTGCTTATAGGCTTTGGTGAAGATAGCACCA GATCTTGTAGTGCTGACTGTGTCAGAATCCAAGGG	3374
	AAGCCTATCAACGAATG	3375
	CATTCGTTGATAGGCTT	3376
Colorectal cancer Val800Leu GTT-CTT	GCCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATG CCATAGAAGACCTCATGGTTGTGCCTGACAAAATCTCCGAAG TTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGA	3377
	TCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTACAACCTTCGGA GATTTTGTGAGGCACAACCATGAGGTCTTCTATGGCATCTAGA CGATCATTAAATAGCATAATGGTTACAGAGTGGGGC	3378
	ACCTCATGGTTGTGCCT	3379
	AGGCACAACCATGAGGT	3380
Colorectal cancer Asp803Gly GAC-GGC	GTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAAGA CCTCATGGTTGTGCCTGACAAAATCTCCGAAGTTGTAGAGCT TCTAAAGAAGCTTCCAGATCTTGAGAGGCTACTCAG	3381
	CTGAGTAGCCTCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTA CAACTTCGGAGATTTTGTGAGGCACAACCATGAGGTCTTCTAT GGCATCTAGACGATCATTAAATAGCATAATGGTTAC	3382
	TGTGCCTGACAAAATCT	3383
	AGATTTTGTGAGGCACA	3384
Non-polypoid colorectal cancer Tyr850Cys TAC-TGC	CTCCCCTGAAGAGTCAGAACCACCCAGACACAGGGGCTATAA TGTATGAAGAACTACATACAGCAAGAAGAAGATTATTGATTT TCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAA	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTACACATTACTTTGAATCCTTCCAGAGCAGAAAGAAAATCAA TAATCTTCTTCTTGCTGTATGTAGTTTCTTCATACATTATAGCC CTGCTGTCTGGGTGGTTCTGACTCTTCAGGGGAG	3385
	AACTACATACAGCAAGA	3386
	TCTTGCTGTATGTAGTT	3387
Colorectal cancer Pro1087Thr CCC-ACC	TATAGTCGAGGGGGGTGATGGTCCTATGTGTGCGCCAGTAATT CTGTTGCCGGAAGATACCCCCCCCTTCTTAGAGCTTAAAGGA TCACGCCATCCTTGCAATACGAAGACTTTTTTTGGAG	3388
	CTCCAAAAAAGTCTTCGTAATGCAAGGATGGCGTGATCCTTT AAGCTCTAAGAAGGGGGGGGTATCTTCCGGCAACAGAATTAC TGGGCGACACATAGGACCATCACCCCCTCGACTATA	3389
	AAGATACCCCCCCCTTC	3390
	GAAGGGGGGGGTATCTT	3391
Non-polyposis colorectal cancer Gln1258Term CAA-TAA	ACTATAAAATGTCGTACATTATTTTCAACTCACTACCATTCATT AGTAGAAGATTATTCTCAAATGTTGCTGTGCGCCTAGGACAT ATGGTATGTCAAATTGTTTTTTCCACAAATTC	3392
	GAATTTGTGGAAAAAACAATTTGCACATACCATATGTCCTAG GCGCACAGCAACATTTTGAGAATAATCTTCTACTAATGAATGG TAGTGAGTTGAAAATAATGTACGACATTTTATAGT	3393
	ATTATTCTCAAATGTT	3394
	AACATTTTGAGAATAAT	3395

EXAMPLE 20

Hyperlipidemia - APOE

Hyperlipidemia is the abnormal elevation of plasma cholesterol and/or triglyceride levels and it is one of the most common diseases. The human apolipoprotein E protein is involved in the transport of endogenous lipids and appears to be crucial for both the direct removal of cholesterol-rich LDL from plasma and conversion of IDL particles to LDL particles. Individuals who either lack apolipoprotein E or who are homozygous for particular alleles of apoE may have have a condition known as dysbetalipoproteinemia, which is characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis.

In a comprehensive review of apoE variants, de Knijff et al., *Hum. Mutat.* 4:178-194 (1994) found that 30 variants had been characterized, including the most common variant, apoE3. To that time, 14 apoE variants had been found to be associated with familial dysbetalipoproteinemia. The

attached table discloses the correcting oligonucleotide base sequences for the APOE oligonucleotides of the invention.

Table 27
APOE Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Apolipoprotein E Glu13Lys cGAG-AAG	TTGTTCCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGT GGAGACAGAGCCGGAGCCCAGCTGCGCCAGCAGACCGAG TGGCAGAGCGGCCAGCGCTGGGAAGTGGCACTGGGTCTGCT	3396
	AGCGACCCAGTGCCAGTTCCCAGCGCTGGCCGCTCTGCCAC TCGGTCTGCTGGCGCAGCTCGGGCTCCGGCTCTGTCTCCAC CGCTTGCTCCACCTTGGCCTGGCATCCTGTGTGGAACAA	3397
	CGGAGCCCAGCTGCGC	3398
	GCGCAGCTCGGGCTCCG	3399
Apolipoprotein E Trp20Term TGGc-TGA	CAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAG CTGCGCCAGCAGACCGAGTGGCAGAGCGGCCAGCGCTGGG AACTGGCACTGGGTCTGCTTTTGGGATTACCTGCGCTGGGTG	3400
	CACCCAGCGCAGGTAATCCCAAAGCGACCCAGTGCCAGTT CCCAGCGCTGGCCGCTCTGCCACTCGGTCTGCTGGCGCAGC TCGGGCTCCGGCTCTGTCTCCACCGCTTGCTCCACCTTG	3401
	ACCGAGTGGCAGAGCGG	3402
	CCGCTCTGCCACTCGGT	3403
Apolipoprotein E Leu28Pro CTG-CCG	CAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGGCA GAGCGGCCAGCGCTGGGAAGTGGCACTGGGTCTGCTTTTGGG ATTACCTGCGCTGGGTGCAGACACTGTCTGAGCAGGTGCA	3404
	TGCACCTGCTCAGACAGTGTCTGCACCCAGCGCAGGTAATCC CAAAGCGACCCAGTGCCAGTTCCCAGCGCTGGCCGCTCTG CCACTCGGTCTGCTGGCGCAGCTCGGGCTCCGGCTCTG	3405
	CTGGGAAGTGGCACTGG	3406
	CCAGTGCCAGTTCCCAG	3407
Apolipoprotein E Cys112Arg gTGC-CGC	CGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGGCTGG GCGCGGACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTA CCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAG G	3408
	CCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCGCCGCGG TACTGCACCAGGCGGCGGCACACGTCTCATGTCCGCGCC CAGCCGGGCTGCGCCGCCTGCAGCTCCTTGACAGCCG	3409
	AGGACGTGTGCGGCGGC	3410
	GCGGCCGCACACGTCT	3411
Apolipoprotein E Gly127Asp GGC-GAC	ACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGG CGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTG CGGGTGCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCG	3412

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGCACCC GCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCG CCGCGGTACTGCACCAGGCGGGCCGCACACGTCTCCATGT	3413
	CATGCTCGGCCAGAGCA	3414
	TGCTCTGGCCGAGCATG	3415
Apolipoprotein E Arg136Cys gCGC-TGC	GTGCAGTACCGCGGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC	3416
	GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC	3417
	TGCGGGTGCGCCTCGCC	3418
	GGCGAGGCGCACCCGCA	3419
Apolipoprotein E Arg136His CGC-CAC	TGCAGTACCGCGGGCGAGGTGCAGGCCATGCTCGGCCAGAG CACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCGC AAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCA	3420
	TGCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTT GCGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTG CTCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCA	3421
	GCGGGTGCGCCTCGCCT	3422
	AGGCGAGGCGCACCCGC	3423
Apolipoprotein E Arg136Ser gCGC-AGC	GTGCAGTACCGCGGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC	3424
	GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC	3425
	TGCGGGTGCGCCTCGCC	3426
	GGCGAGGCGCACCCGCA	3427
Apolipoprotein E Arg142Cys gCGC-TGC	GTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGG TGCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTC CTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT	3428
	AACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAGG AGCCGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGCA CCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCAC	3429
	CCACCTGCGCAAGCTG	3430
	CAGCTTGCGCAGGTGGG	3431
Apolipoprotein E Arg142Leu CGC-CTC	TGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGT GCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCC TCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT	3432
	TAACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAG GAGCCGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGC ACCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCA	3433
	CCACCTGCGCAAGCTGC	3434

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCAGCTTGCGCAGGTGG	3435
Apolipoprotein E Arg145Cys gCGT-TGT	ATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCG	3436
	CCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGAT	
	GCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCG	
	CGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGCA	3437
	TCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGG	
	CGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCAT	
	GCAAGCTGCGTAAGCGG	3438
	CCGCTTACGCAGCTTGC	3439
Apolipoprotein E Arg145Pro CGT-CCT	TGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGC	3440
	CTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATG	
	CCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGG	
	CCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGC	3441
	ATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAG	
	GCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCA	
	CAAGCTGCGTAAGCGGC	3442
	GCCGCTTACGCAGCTTG	3443
Apolipoprotein E Lys146Gln tAAG-CAG	CTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCT	3444
	CCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCC	
	GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG	
	CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG	3445
	GCATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGA	
	GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG	
	AGCTGCGTAAGCGGCTC	3446
	GAGCCGCTTACGCAGCT	3447
Apolipoprotein E Lys146Glu tAAG-GAG	CTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCT	3448
	CCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCC	
	GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG	
	CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG	3449
	GCATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGA	
	GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG	
	AGCTGCGTAAGCGGCTC	3450
	GAGCCGCTTACGCAGCT	3451
Apolipoprotein E Arg158Cys gCGC-TGC	GCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGA	3452
	TGCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCG	
	GGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCC	
	GGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCC	3453
	GGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGCAT	
	CGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGGC	
	TGCAGAAGCGCCTGGCA	3454
	TGCCAGGCGCTTCTGCA	3455

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Apolipoprotein E Gln187Glu aCAG-GAG	CGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGC GCCTGGGGCCCCTGGTGGAA <u>C</u> AGGGCCGCGTGCGGGCCGC CACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGG G	3456
	CCCGCTCCTGTAGCGGCTGGCCGGCCAGGGAGCCACAGT GGCGGCCCGCACGCGGCCCT <u>G</u> TTCCACCAGGGGCCCCAGG CGCTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGC G	3457
	TGGTGGAA <u>C</u> AGGGCCGC	3458
	GCGGCCCT <u>G</u> TTCCACCA	3459
Apolipoprotein E Trp210Term TGG-TAG	TGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCT ACAGGAGCGGGCCCAGGCCT <u>G</u> GGGCGAGCGGCTGCGCGC GCGGATGGAGGAGATGGGCAGCCGGACCCGCGACCGCCTG GA	3460
	TCCAGGCGGTGCGGGTCCGGCTGCCATCTCCTCCATCCG CGCGCGCAGCCGCTCGCCC <u>A</u> GGCCTGGGCCCGCTCCTGT AGCGGCTGGCCGGCCAGGGAGCCACAGTGGCGGGCCCGCA CCAGGCCT <u>G</u> GGGCGAGC	3461
	CCAGGCCT <u>G</u> GGGCGAGC	3462
	GCTCGCCCC <u>A</u> GGCCTGG	3463
Apolipoprotein E Arg228Cys cCGC-TGC	CAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAGA TGGGCAGCCGGACCCGCGAC <u>C</u> GCCTGGACGAGGTGAAGGA GCAGGTGGCGGAGGTGCGCGCCAAGCTGGAGGAGCAGGCC C	3464
	GGGCCTGCTCCTCCAGCTTGGCGCGCACCTCCGCCACCTGC TCCTTCACCTCGTCCAGGC <u>G</u> GTCGCGGGTCCGGCTGCCCAT CTCCTCCATCCGCGCGCGCAGCCGCTCGCCCCAGGCCTG	3465
	CCGCGACCGCCTGGAC	3466
	GTCCAGGCGGTGCGGG	3467
Apolipoprotein E Glu244Lys gGAG-AAG	CGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGG CGGAGGTGCGCGCCAAGCTG <u>G</u> AGGAGCAGGCCCAGCAGAT ACGCCTGCAGGCCGAGGCCTTCCAGGCCCGCCTCAAGAGCT	3468
	AGCTCTTGAGGCGGGCCTGGAAGGCCTCGGCCTGCAGGCGT ATCTGCTGGGCCTGCTCCTC <u>C</u> AGCTTGGCGCGCACCTCCGC CACCTGCTCCTTCACCTCGTCCAGGCGGTGCGGGTCCG	3469
	CCAAGCTG <u>G</u> AGGAGCAG	3470
	CTGCTCCTC <u>C</u> AGCTTGG	3471

EXAMPLE 21**Familial hypercholesterolemia - LDLR**

Familial hypercholesterolemia is characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL) and is, hence, one of the conditions producing a hyperlipoproteinemia phenotype. Familial hypercholesterolemia is an autosomal dominant disorder characterized by elevation

of serum cholesterol bound to low density lipoprotein (LDL). Mutations in the LDL receptor (LDLR) gene cause this disorder. The attached table discloses the correcting oligonucleotide base sequences for the LDLR oligonucleotides of the invention.

Table 28
LDLR Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Glu10Term cGAG-TAG	GCGTTGAGAGACCCTTTCTCCTTTTCCTCTCTCTCAGTGGGC GACAGATGCGAAAGAAACGAGTTCCAGTGCCAAGACGGGAA ATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTG	3472
	CAGCGCTGCCATCGCAGACCCACTTGTAGGAGATGCATTTCC CGTCTTGGCACTGGAACCTGTTTCTTTTCGCATCTGTGCCCCA CTGAGAGAGAGGAAAAGGAGAAAGGGTCTCTCAACGC	3473
	AAAGAAACGAGTTCCAG	3474
	CTGGAACCTGTTTCTTT	3475
Hypercholesterolaemia Gln12Term cCAG-TAG	AGAGACCCTTTCTCCTTTTCCTCTCTCTCAGTGGGCGACAGA TGCGAAAGAAACGAGTTCCAGTGCCAAGACGGGAAATGCATC TCCTACAAGTGGGTCTGCGATGGCAGCGCTGAGTGCC	3476
	GGCACTCAGCGCTGCCATCGCAGACCCACTTGTAGGAGATG CATTTCCCGTCTTGGCACTGGAACCTGTTTCTTTTCGCATCTGT CGCCCACTGAGAGAGAGGAAAAGGAGAAAGGGTCTCT	3477
	ACGAGTTCCAGTGCCAA	3478
	TTGGCACTGGAACCTCGT	3479
Hypercholesterolaemia Gln14Term cCAA-TAA	CCTTTCTCCTTTTCCTCTCTCTCAGTGGGCGACAGATGCGAA AGAAACGAGTTCCAGTGCCAAGACGGGAAATGCATCTCCTAC AAGTGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATG	3480
	CATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTTGTAG GAGATGCATTTCCCGTCTTGGCACTGGAACCTGTTTCTTTTCG CATCTGTGCCCCACTGAGAGAGAGGAAAAGGAGAAAGG	3481
	TCCAGTGCCAAGACGGG	3482
	CCCGTCTTGGCACTGGA	3483
Hypercholesterolaemia Trp23Term TGG-TAG	GCGACAGATGCGAAAGAAACGAGTTCCAGTGCCAAGACGGG AAATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTGAG TGCCAGGATGGCTCTGATGAGTCCCAGGAGACGTGCTG	3484
	CAGCACGTCTCCTGGGACTCATCAGAGCCATCCTGGCACTCA GCGCTGCCATCGCAGACCCACTTGTAGGAGATGCATTTCCCG TCTTGGCACTGGAACCTGTTTCTTTTCGCATCTGTGCGC	3485
	CTACAAGTGGGTCTGCG	3486
	CGCAGACCCACTTGTAG	3487
Hypercholesterolaemia Ala29Ser cGCT-TCT	AACGAGTTCCAGTGCCAAGACGGGAAATGCATCTCCTACAAG TGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGA TGAGTCCCAGGAGACGTGCTGTGAGTCCCCTTTGGGCA	3488

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGCCCAAAGGGGACTCACAGCACGTCTCCTGGGACTCATCA GAGCCATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTT GTAGGAGATGCATTTCCCGTCTTGGCACTGGAACTCGTT	3489
	ATGGCAGCGCTGAGTGC	3490
	GCACTCAGCGCTGCCAT	3491
Hypercholesterolaemia Cys31Tyr TGC-TAC	TCCAGTGCCAAGACGGGAAATGCATCTCCTACAAGTGGGTCT GCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGATGAGTCC CAGGAGACGTGCTGTGAGTCCCCTTTGGGCATGATATG	3492
	CATATCATGCCCAAAGGGGACTCACAGCACGTCTCCTGGGAC TCATCAGAGCCATCCTGGCACTCAGCGCTGCCATCGCAGAC CCACTTGTAGGAGATGCATTTCCCGTCTTGGCACTGGA	3493
	CGCTGAGTGCCAGGATG	3494
	CATCCTGGCACTCAGCG	3495
Hypercholesterolaemia Arg57Cys cCGT-TGT	AATCCTGTCTCTTCTGTAGTGTCTGTCACCTGCAAATCCGGG GACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATTCCTCA GTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAACG	3496
	CGTTGTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAG GAATGCAGCGGTTGACACGGCCCCACAGCTGAAGTCCCCG GATTTGCAGGTGACAGACACTACAGAAGAGACAGGATT	3497
	GTGGGGGCGGTGTCAAC	3498
	GTTGACACGGCCCCCAC	3499
Hypercholesterolaemia Gln64Term tCAG-TAG	TCTGTCACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCGG TGTC AACCGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCA AGTGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTC	3500
	GACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCACTTGGC CATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGACACGG CCCCACAGCTGAAGTCCCCGGATTTGCAGGTGACAGA	3501
	GCATTCCTCAGTTCTGG	3502
	CCAGAACTGAGGAATGC	3503
Hypercholesterolaemia Trp66Gly cTGG-GGG	ACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCGGTGTCAA CCGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGG ACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGT	3504
	ACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCA CTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGGT	3505
	CTCAGTTCTGGAGGTGC	3506
	GCACCTCCAGAACTGAG	3507
Hypercholesterolaemia Trp66Term TGG-TAG	CCTGCAAATCCGGGGACTTCAGCTGTGGGGGCGGTGTCAAC CGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTG	3508
	CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGG	3509
	TCAGTTCTGGAGGTGCG	3510

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CGCACCTCCAGAACTGA	3511
Hypercholesterolaemia Cys68Arg gTGC-CGC	AAATCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTG	3512
	CATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGA	
	CAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCC	
	GGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCG	3513
	AGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAG	
	CGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGATT	
	TCTGGAGGTGCGATGGC	3514
	GCCATCGCACCTCCAGA	3515
Hypercholesterolaemia Cys68Trp TGCg-TGG	ATCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCA	3516
	TTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA	
	ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCT	
	AGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTC	3517
	GCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA	
	GCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGAT	
	TGGAGGTGCGATGGCCA	3518
	TGGCCATCGCACCTCCA	3519
Hypercholesterolaemia Cys68Tyr TGC-TAC	AATCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGC	3520
	ATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGAC	
	AACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC	
	GGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTC	3521
	GCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA	
	GCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGATT	
	CTGGAGGTGCGATGGCC	3522
	GGCCATCGCACCTCCAG	3523
Hypercholesterolaemia Asp69Asn cGAT-AAT	TCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCAT	3524
	TCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA	
	ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG	
	CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT	3525
	CGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATG	
	CAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGA	
	GGAGGTGCGATGGCCAA	3526
	TTGGCCATCGCACCTCC	3527
Hypercholesterolaemia Asp69Gly GAT-GGT	CCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATT	3528
	CCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAA	
	CGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGC	
	GCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTT	3529
	GTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAAT	
	GCAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGG	
	GAGGTGCGATGGCCAAAG	3530
	CTTGGCCATCGCACCTC	3531
Hypercholesterolaemia Asp69Tyr cGAT-TAT	TCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCAT	3532
	TCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA	
	ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATG CAGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGGA	3533
	GGAGGTGCGATGGCCAA	3534
	TTGGCCATCGCACCTCC	3535
Hypercholesterolaemia Gln71Glu cCAA-GAA	GACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATTCTCTCA GTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAACGGCT CAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGCCTTTG	3536
	CAAAGGCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAG CCGTTGTCGCAGTCCACTTGCCATCGCACCTCCAGAACTGA GGAATGCAGCGGTTGACACGGCCCCACAGCTGAAGTC	3537
	GCGATGGCCAAGTGGAC	3538
	GTCCACTTGCCATCGC	3539
Hypercholesterolaemia Cys74Gly cTGC-GGC	TGTGGGGGCGGTGTCAACCGCTGCATTCTCTGAG GTGCGATGGCCAAGTGGACTGCGACAACGGCTCAGACGAGC AAGGCTGTCGTAAGTGTGGCCCTGCCTTTGCTATTGAGC	3540
	GCTCAATAGCAAAGGCAGGGCCACACTTACGACAGCCTTGCT CGTCTGAGCCGTTGTCGCAGTCCACTTGCCATCGCACCTC CAGAACTGAGGAATGCAGCGGTTGACACGGCCCCCACA	3541
	AAGTGGACTGCGACAAC	3542
	GTTGTCGCAGTCCACTT	3543
Hypercholesterolaemia Ser78Term TCA-TGA	TCAACCGCTGCATTCTCTGAGGTGCGATGGCCAAG TGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAG TGTGGCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCT	3544
	AGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCACACTTA CGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCACTTGG CCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGA	3545
	CAACGGCTCAGACGAGC	3546
	GCTCGTCTGAGCCGTTG	3547
Hypercholesterolaemia Glu80Lys cGAG-AAG	CGCTGCATTCTCTGAGGTGCGATGGCCAAGTGG CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA	3548
	TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG	3549
	GCTCAGACGAGCAAGGC	3550
	GCCTTGCTCGTCTGAGC	3551
Hypercholesterolaemia Glu80Term cGAG-TAG	CGCTGCATTCTCTGAGGTGCGATGGCCAAGTGG CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA	3552
	TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG	3553
	GCTCAGACGAGCAAGGC	3554

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Gln81Term gCAA-TAA	GCCTTGCTCGTCTGAGC	3555
	TGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGC	3556
	GACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC	
	TGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGAGTG	
	CACTCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGG	3557
	CCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAG	
Hypercholesterolaemia Cys88Arg gTGC-CGC	TCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA	
	CAGACGAGCAAGGCTGT	3558
	ACAGCCTTGCTCGTCTG	3559
	TGGGAGACTTCACACGGTGATGGTGGTCTCGGCCCATCCAT	3560
	CCCTGCAGCCCCAAGACGTGCTCCAGGACGAGTTTCGCT	
	GCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTCTGTG	
Hypercholesterolaemia Glu92Term cGAG-TAG	CACAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAG	3561
	CGAAACTCGTCCTGGGAGCACGTCTTGGGGGCTGCAGGGAT	
	GGATGGGCCGAGACCACCATCACCGTGTGAAGTCTCCCA	
	CCAAGACGTGCTCCCAG	3562
	CTGGGAGCACGTCTTGG	3563
	CACGGTGATGGTGGTCTCGGCCCATCCATCCCTGCAGCCCC	3564
Hypercholesterolaemia Cys95Arg cTGC-CGC	CAAGACGTGCTCCAGGACGAGTTTCGCTGCCACGATGGGA	
	AGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGG	
	CCCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTTC	3565
	CCATCGTGGCAGCGAAACTCGTCCTGGGAGCACGTCTTGGG	
	GGCTGCAGGGATGGATGGGCCGAGACCACCATCACCGTG	
	CCCAGGACGAGTTTCGC	3566
Hypercholesterolaemia Asp97Tyr cGAT-TAT	GCGAAACTCGTCCTGGG	3567
	GGTGGTCTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTG	3568
	CTCCCAGGACGAGTTTCGCTGCCACGATGGGAAGTGCATCT	
	CTCGGCAGTTCGTCTGTGACTCAGACCGGGACTGCTTGG	
	CCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGAGAG	3569
	ATGCACTTCCCATCGTGGCAGCGAAACTCGTCCTGGGAGCA	
Hypercholesterolaemia Trp(-12)Arg cTGG-AGG	CGTCTTGGGGGCTGCAGGGATGGATGGGCCGAGACCACC	
	AGTTTCGCTGCCACGAT	3570
	ATCGTGGCAGCGAAACT	3571
	CTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTGCTCCA	3572
	GGACGAGTTTCGCTGCCACGATGGGAAGTGCATCTCTCGGC	
	AGTTCGTCTGTGACTCAGACCGGGACTGCTTGGACGGCT	
Hypercholesterolaemia Trp(-12)Arg cTGG-AGG	AGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGC	3573
	CGAGAGATGCACTTCCCATCGTGGCAGCGAAACTCGTCCTG	
	GGAGCACGTCTTGGGGGCTGCAGGGATGGATGGGCCGAG	
	GCTGCCACGATGGGAAG	3574
	CTTCCCATCGTGGCAGC	3575
	GGGTGCGGACACTGCCTGGCAGAGGCTGCGAGCATGGGGC	3576
Hypercholesterolaemia Trp(-12)Arg cTGG-AGG	CCTGGGGCTGGAAATTGCGCTGGACCGTCGCCTTGCTCCTC	
	GCCGCGGCGGGGACTGCAGGTAAGGCTTGCTCCAGGCGCC	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGCGCCTGGAGCAAGCCTTACCTGCAGTCCCCGCCGCGGC GAGGAGCAAGGCGACGGTCCAGCGCAATTTCCAGCCCCAGG GCCCCATGCTCGCAGCCTCTGCCAGGCAGTGTCCCGACCC	3577
	AATTGCGCTGGACCGTC	3578
	GACGGTCCAGCGCAATT	3579
Hypercholesterolaemia Trp(-18)Term TGGg-TGA	CAGCAGGTCGTGATCCGGGTCTGGGACACTGCCTGGCAGAGG CTGCGAGCATGGGGCCCTGGGGCTGGAAATTGCGCTGGACC GTCGCCTTGCTCCTCGCCGCGGCGGGGACTGCAGGTAAG	3580
	CTTACCTGCAGTCCCCGCCGCGGCGAGGAGCAAGGCGACG GTCCAGCGCAATTTCCAGCCCAGGGCCCCATGCTCGCAGC CTCTGCCAGGCAGTGTCCCGACCCGATCACGACCTGCTG	3581
	GGGCCCTGGGGCTGGAA	3582
	TTCCAGCCCAGGGCCC	3583
Hypercholesterolaemia Met(-21)Leu cATG-TTG	CAGCTAGGACACAGCAGGTCGTGATCCGGGTCTGGGACACTG CCTGGCAGAGGCTGCGAGCATGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA	3584
	TCCCCGCCGCGGCGAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCATGCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG	3585
	CTGCGAGCATGGGGCCC	3586
	GGGCCCCATGCTCGCAG	3587
Hypercholesterolaemia Met(-21)Val cATG-GTG	CAGCTAGGACACAGCAGGTCGTGATCCGGGTCTGGGACACTG CCTGGCAGAGGCTGCGAGCATGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA	3588
	TCCCCGCCGCGGCGAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCATGCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG	3589
	CTGCGAGCATGGGGCCC	3590
	GGGCCCCATGCTCGCAG	3591
Hypercholesterolaemia Ile101Phe cATC-TTC	ATCCCTGCAGCCCCAAGACGTGCTCCCAGGACGAGTTTCG CTGCCACGATGGGAAGTGCACTCTCTCGGCAGTTCGTCTGTGA CTCAGACCGGGACTGCTTGACGGCTCAGACGAGGCCT	3592
	AGGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA CAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCG AAACTCGTCCTGGGAGCACGTCTTGGGCTGCAGGGAT	3593
	GGAAGTGCACTCTCTCGG	3594
	CCGAGAGATGCACTTCC	3595
Hypercholesterolaemia Gln104Term gCAG-TAG	GCCCCAAGACGTGCTCCCAGGACGAGTTTCGCTGCCACGA TGGAAGTGCACTCTCTCGGCAGTTCGTCTGTGACTCAGACCG GGAAGTGGTGGACGGCTCAGACGAGGCCTCCTGCCCGG	3596
	CCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTCCCG GTCTGAGTCACAGACGAACTGCCGAGAGATGCACTTCCCATC GTGGCAGCGAAACTCGTCCTGGGAGCACGTCTTGGGGGC	3597
	TCTCTCGGCAGTTCGTC	3598

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GACGAACTGCCGAGAGA	3599
Hypercholesterolaemia Cys113Arg cTGC-CGC	TTTCGCTGCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTC	3600
	TGTGACTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGC	
	CTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTCC	
	GGAAGCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGC	3601
	CTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGA	
	CGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCGAAA	
	ACCGGGACTGCTTGGAC	3602
	GTCCAAGCAGTCCCGGT	3603
Hypercholesterolaemia Glu119Lys cGAG-AAG	AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC	3604
	TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC	
	CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT	
	AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG	3605
	AGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTC	
	CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT	
	GCTCAGACGAGGCCTCC	3606
	GGAGGCCTCGTCTGAGC	3607
Hypercholesterolaemia Glu119Term cGAG-TAG	AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC	3608
	TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC	
	CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT	
	AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG	3609
	AGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTC	
	CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT	
	GCTCAGACGAGGCCTCC	3610
	GGAGGCCTCGTCTGAGC	3611
Hypercholesterolaemia Cys122Term TGc-TGA	TCGGCAGTTCGTCTGTGACTCAGACCGGGACTGCTTGGACG	3612
	GCTCAGACGAGGCCTCCTGCCCGGTGCTCACCTGTGGTCCC	
	GCCAGCTTCCAGTGCAACAGCTCCACCTGCATCCCCCAG	
	CTGGGGGATGCAGGTGGAGCTGTTGCACTGGAAGCTGGCGG	3613
	GACCACAGGTGAGCACCGGGCAGGAGGCCTCGTCTGAGCC	
	GTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGA	
	GCCTCCTGCCCGGTGCT	3614
	AGCACCGGGCAGGAGGC	3615
Hypercholesterolaemia Cys127Trp TGTg-TGG	TGACTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGCCT	3616
	CCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTCCAGTGC	
	AACAGCTCCACCTGCATCCCCCAGCTGTGGGCCTGCGAC	
	GTCGCAGGCCACAGCTGGGGGATGCAGGTGGAGCTGTTGC	3617
	ACTGGAAGCTGGCGGGACCACAGGTGAGCACCGGGCAGGA	
	GGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA	
	CTCACCTGTGGTCCCGC	3618
	GCGGGACCACAGGTGAG	3619
Hypercholesterolaemia Gln133Term cCAG-TAG	TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC	3620
	CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCAT	
	CCCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCG	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGCAGTCGGGGTCGTTGTCGCAGGCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGG TGAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCA CCAGCTTCCAGTGCAAC	3621
	GTTGCACTGGAAGCTGG	3622
		3623
Hypercholesterolaemia Cys134Gly gTGC-GGC	TTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCACCTG TGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATCC CCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG CTTCGCAGTCGGGGTCGTTGTCGCAGGCCACAGCTGGGGG ATGCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA GGTGAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAA GCTTCCAGTGCAACAGC	3624
	GCTGTTGCACTGGAAGC	3625
		3626
		3627
Hypercholesterolaemia Cys139Gly cTGC-GGC	GAGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTT CCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGT ACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCAG GCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA GCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCTC GCTCCACCTGCATCCCC	3628
	GGGGATGCAGGTGGAGC	3629
		3630
		3631
Hypercholesterolaemia Cys139Tyr TGC-TAC	AGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTC CAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCTG CGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGTG CACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCA GGCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGA AGCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCT CTCCACCTGCATCCCC	3632
	GGGGGATGCAGGTGGAG	3633
		3634
		3635
Hypercholesterolaemia Cys146Term TGCg-TGA	CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCAT CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG ATGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTT AAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTTC GCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAG TGGGCCTGCGACAACGA	3636
	TCGTTGTCGCAGGCCCA	3637
		3638
		3639
Hypercholesterolaemia Asp147Asn cGAC-AAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA GGGCCTGCGACAACGAC	3640
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		3642

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTCGTTGTGCGCAGGCC	3643
Hypercholesterolaemia Asp147His cGAC-CAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3644
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGCAGGCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA GGGCCTGCGACAACGAC	3645
	GTCGTTGTGCGCAGGCC	3646
		3647
		3648
Hypercholesterolaemia Asp147Tyr cGAC-TAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3649
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGCAGGCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA GGGCCTGCGACAACGAC	3650
	GTCGTTGTGCGCAGGCC	3651
		3652
		3653
Hypercholesterolaemia Cys152Arg cTGC-CGC	TTCCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGC CTGCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGT GGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG	3654
	CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTGCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA ACCCCGACTGCGAAGAT	3655
	ATCTTCGCAGTCGGGGT	3656
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		3658
Hypercholesterolaemia Cys152Gly cTGC-GGC	TTCCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGC CTGCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGT GGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG	3659
	CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTGCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA ACCCCGACTGCGAAGAT	3660
	ATCTTCGCAGTCGGGGT	3661
		3662
		3663
Hypercholesterolaemia Cys152Trp TGCg-TGG	CCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGTGG CCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGAC	3664
	GTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCC ACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTGCGCAG GCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGG CCCGACTGCGAAGATGG	3665
	CCATCTTCGCAGTCGGG	3666
		3667
		3668
Hypercholesterolaemia Asp154Asn aGAT-AAT	TGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCTGCGA CAACGACCCCGACTGCGAAGATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGACAGTA	3669
		3670

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TACTGTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCTG CAGGCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCA	3665
	ACTGCGAAGATGGCTCG	3666
	CGAGCCATCTTCGCAGT	3667
Hypercholesterolaemia Ser156Leu TCG-TTG	GCTCCACCTGCATCCCCAGCTGTGGGCCTGCGACAACGAC CCCGACTGCGAAGATGGCTCGGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTTCCAAGGGGACAGTAGCCCCTG	3668
	CAGGGGCTACTGTCCCCTTGGAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCCGAGCCATCTTCGCAGTCGGGGTC GTTGTCTGCAGGCCACAGCTGGGGGATGCAGGTGGAGC	3669
	AGATGGCTCGGATGAGT	3670
	ACTCATCCGAGCCATCT	3671
Hypercholesterolaemia Cys163Tyr TGT-TAT	TGTGGGCCTGCGACAACGACCCCGACTGCGAAGATGGCTCG GATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAA GGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG	3672
	CAGTGGAAGTGAAGGCCGAGCAGGGGCTACTGTCCCCTTG GAACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG AGCCATCTTCGCAGTCGGGGTCGTTGTCTGCAGGCCACACA	3673
	GCAGCGCTGTAGGGGTC	3674
	GACCCCTACAGCGCTGC	3675
Hypercholesterolaemia Tyr167Term TACg-TAG	CAACGACCCCGACTGCGAAGATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGACAGTAGC CCCTGCTCGGCCTTCGAGTTCCACTGCCTAAGTGGCGAG	3676
	CTCGCCACTTAGGCAGTGGAAGTGAAGGCCGAGCAGGGGC TACTGTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTG	3677
	GGTCTTTACGTGTTCCA	3678
	TGGAACACGTAAAGACC	3679
Hypercholesterolaemia Gln170Term cCAA-TAA	CCCGACTGCGAAGATGGCTCGGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTTCCAAGGGGACAGTAGCCCCTGCTC GGCCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCC	3680
	GGATGCACTCGCCACTTAGGCAGTGGAAGTGAAGGCCGAG CAGGGGCTACTGTCCCCTTGGAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCCGAGCCATCTTCGCAGTCGGG	3681
	ACGTGTTCCAAGGGGAC	3682
	GTCCCCTTGGAACACGT	3683
Hypercholesterolaemia Cys176Phe TGC-TTC	CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTT CAAGGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA	3684
	TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAAGTGAAGGCCGAGCAGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG	3685
	TAGCCCCTGCTCGGCCT	3686

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Cys176Tyr TGC-TAC	AGGCCGAGCAGGGGCTA	3687
	CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCC CAAGGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA	3688
	TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAAGTCTGAAGGCCGAGCAGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG	3689
	TAGCCCCTGCTCGGCCT	3690
	AGGCCGAGCAGGGGCTA	3691
	ATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAG GGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTGCCTA AGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGG	3692
Hypercholesterolaemia Ser177Leu TCG-TTG	CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAG GCAGTGGAAGTCTGAAGGCCGAGCAGGGGCTACTGTCCCCTT GGAACACGTAAAGACCCCTACAGCGCTGCGGCCACTCAT	3693
	CCCCTGCTCGGCCTTCG	3694
	CGAAGGCCGAGCAGGGG	3695
	TACGTGTTCCAAGGGGACAGTAGCCCCTGCTCGGCCTTCGA GTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACG	3696
Hypercholesterolaemia Glu187Lys cGAG-AAG	CGTCAGATTTGTCCTTGCACTCGGGGCCACCATCACAGCGC CAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGTCT GAAGGCCGAGCAGGGGCTACTGTCCCCTTGGAACACGTA	3697
	TAAGTGGCGAGTGCATC	3698
	GATGCACTCGCCACTTA	3699
	CAAGGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATG GTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAACT	3700
Hypercholesterolaemia His190Tyr cCAC-TAC	AGTTTTCCTCGTCAGATTTGTCCTTGCACTCGGGGCCACCAT CACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAG TGGAAGTCTGAAGGCCGAGCAGGGGCTACTGTCCCCTTG	3701
	AGTGCATCCACTCCAGC	3702
	GCTGGAGTGGATGCACT	3703
	CCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCA GCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCT GACGAGGAAACTGCGGTATGGGCGGGGCCAGGGTGGG	3704
Hypercholesterolaemia Gly198Asp GGC-GAC	CCCACCCTGGCCCCGCCATACCGCAGTTTTCTCGTCAGAT TTGTCCTTGCACTCGGGGCCACCATCACAGCGCCAGCTGGA GTGGATGCACTCGCCACTTAGGCAGTGGAAGTCTGAAGG	3705
	TGATGGTGGCCCCGACT	3706
	AGTCGGGGCCACCATCA	3707
	GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTG GCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACG AGGAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG	3708

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCG TCAGATTTGTCCTTGCACTGGGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGTC	3709
	GTGGCCCCGACTGCAAG	3710
	CTTGCACTCGGGGCCAC	3711
Hypercholesterolaemia Asp200Gly GAC-GGC	AGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAG GAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGG	3712
	CCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTC GTCAGATTTGTCCTTGCACTCGGGGCCACCATCACAGCGCCA GCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGTC	3713
	TGGCCCCGACTGCAAGG	3714
	CCTTGCACTCGGGGCCA	3715
Hypercholesterolaemia Asp200Tyr cGAC-TAC	GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTG GCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACG AGGAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG	3716
	CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCG TCAGATTTGTCCTTGCACTGGGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGTC	3717
	GTGGCCCCGACTGCAAG	3718
	CTTGCACTCGGGGCCAC	3719
Hypercholesterolaemia Cys201Term TGCa-TGA	CCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCT GTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGT	3720
	ACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTT CCTCGTCAGATTTGTCCTTGCACTCGGGGCCACCATCACAGC GCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGG	3721
	CCCGACTGCAAGGACAA	3722
	TTGTCCTTGCACTCGGG	3723
Hypercholesterolaemia Cys201Tyr TGC-TAC	TCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGC TGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCG	3724
	CGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTT CTCGTCAGATTTGTCCTTGCACTCGGGGCCACCATCACAGCG CCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGA	3725
	CCCCGACTGCAAGGACA	3726
	TGTCCTTGCACTCGGG	3727
Hypercholesterolaemia Asp203Asn gGAC-AAC	TGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA TGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAACT GCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTA	3728
	TAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCTCGTCAGATTTGTCCTTGCACTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA	3729
	ACTGCAAGGACAAATCT	3730

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AGATTTGTCCTTGCAGT	3731
Hypercholesterolaemia Asp203Gly GAC-GGC	GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAACTG CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT	3732
	ATAGGACGCCCCGCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC	3733
	CTGCAAGGACAAATCTG	3734
	CAGATTTGTCCTTGCAG	3735
		3736
Hypercholesterolaemia Asp203Val GAC-GTC	GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAACTG CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT	3737
	ATAGGACGCCCCGCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC	3738
	CTGCAAGGACAAATCTG	3739
	CAGATTTGTCCTTGCAG	3740
		3741
Hypercholesterolaemia Ser205Pro aTCT-CCT	AGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGG CCCCGACTGCAAGGACAAATCTGACGAGGAAACTGCGGTAT GGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCT	3742
	AGGTGATAGGACGCCCCGCCCCACCCTGGCCCCGCCATA CCGCAGTTTTCTCGTCAGATTTGTCCTTGCAGTCGGGGCCA CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACT	3743
	AGGACAAATCTGACGAG	3744
	CTCGTCAGATTTGTCCT	3745
		3746
Hypercholesterolaemia Asp206Glu GACg-GAG	CGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCG ACTGCAAGGACAAATCTGACGAGGAAACTGCGGTATGGGC GGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCC	3747
	GGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCCG CCCATACCGCAGTTTTCTCGTCAGATTTGTCCTTGCAGTCG GGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCG	3748
	AAATCTGACGAGGAAAA	3749
	TTTTCTCGTCAGATTT	3750
		3751
Hypercholesterolaemia Glu207Gln cGAG-CAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGACGAGGAAACTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3752
	AGGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTCGTCAGATTTGTCCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3753
	AATCTGACGAGGAAAC	3754
	GTTTTCTCGTCAGATT	3755
		3756

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Glu207Lys cGAG-AAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGACGAGGAAACTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3752
	AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTCGTCAGATTTGTCCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3753
	AATCTGACGAGGAAAC	3754
	GTTTTCTCGTCAGATT	3755
Hypercholesterolaemia Glu207Term cGAG-TAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGACGAGGAAACTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3756
	AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTCGTCAGATTTGTCCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3757
	AATCTGACGAGGAAAC	3758
	GTTTTCTCGTCAGATT	3759
Hypercholesterolaemia Glu219Lys cGAA-AAA	TCTTGAGAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGG CCACCTGTGCGCCTGACGAATTCCAGTGCTCTGATGGAAACT GCATCCATGGCAGCCGGCAGTGTGACCGGGAATATG	3760
	CATATTCGCGGTCACTGCCGGCTGCCATGGATGCAGTTTC CATCAGAGCACTGGAATTCGTCAGGGCGACAGGTGGCCACA GCTGGAAAACAGGACAGAGTGTGTTGATTTCTCAAGA	3761
	GCCCTGACGAATTCCAG	3762
	CTGGAATTCGTCAGGGC	3763
Hypercholesterolaemia Gln221Term cCAG-TAG	GAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGGCCACCT GTCGCCCTGACGAATTCAGTGCTCTGATGGAAACTGCATCC ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCA	3764
	TGCAGTCATATTCGCGGTCACTGCCGGCTGCCATGGATGC AGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGACAGGTGG CCACAGCTGGAAAACAGGACAGAGTGTGTTGATTTTC	3765
	ACGAATTCAGTGCTCT	3766
	AGAGCACTGGAATTCGT	3767
Hypercholesterolaemia Cys227Phe TGC-TTC	CCTGTTTTCCAGCTGTGGCCACCTGTCGCCCTGACGAATTCC AGTGCTCTGATGGAAACTGCATCCATGGCAGCCGGCAGTGT GACCGGGAATATGACTGCAAGGACATGAGCGATGAAGT	3768
	ACTTCATCGCTCATGTCCTTGCAGTCATATTCGCGGTCACT GCCGGCTGCCATGGATGCAGTTTCCATCAGAGCACTGGAATT CGTCAGGGCGACAGGTGGCCACAGCTGGAAAACAGG	3769
	TGGAAACTGCATCCATG	3770
	CATGGATGCAGTTTCCA	3771
Hypercholesterolaemia Asp235Glu GACc-GAA	TCGCCCTGACGAATTCAGTGCTCTGATGGAAACTGCATCCA TGGCAGCCGGCAGTGTGACCGGGAATATGACTGCAAGGACA TGAGCGATGAAGTTGGCTGCGTTAATGGTGAAGCGCTGG	3772

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	CCAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCATGTC CTTGCAAGTCATATTCCCGGTCACACTGCCGGCTGCCATGGAT GCAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGA CAGTGTGACCGGGAATA	3773
	TATTCCCGGTCACACTG	3774
		3775
		3776
Hypercholesterolaemia Asp235Gly GAC-GGC	GTCGCCCTGACGAATTCCAGTGCTCTGATGGAACTGCATCC ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTG CAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCATGTCC TTGCAGTCATATTCCCGGTCACACTGCCGGCTGCCATGGATG CAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGAC	3777
	GCAGTGTGACCGGGAAT	3778
	ATTCCCGGTCACACTGC	3779
		3780
Hypercholesterolaemia Glu237Lys gGAA-AAA	CCTGACGAATTCCAGTGCTCTGATGGAACTGCATCCATGGC AGCCGGCAGTGTGACCGGGAATATGACTGCAAGGACATGAG CGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGGCCAT ATGGCCAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCA TGTCTTGCAGTCATATTCCCGGTCACACTGCCGGCTGCCAT GGATGCAGTTTCCATCAGAGCACTGGAATTCGTCAGG	3781
	GTGACCGGGAATATGAC	3782
	GTCATATTCCCGGTCAC	3783
		3784
Hypercholesterolaemia Cys240Phe TGC-TTC	TCCAGTGCTCTGATGGAACTGCATCCATGGCAGCCGGCAGT GTGACCGGGAATATGACTGCAAGGACATGAGCGATGAAGTTG GCTGCGTTAATGGTGAGCGCTGGCCATCTGGTTTTCC GGAAAACCAGATGGCCAGCGCTCACCATTAAACGCAGCCAACT TCATCGCTCATGTCTTGCAGTCATATTCCCGGTCACACTGC CGGCTGCCATGGATGCAGTTTCCATCAGAGCACTGGA	3785
	ATATGACTGCAAGGACA	3786
	TGTCCTTGCAGTCATAT	3787
		3788
Hypercholesterolaemia Asp245Glu GATg-GAA	AAACTGCATCCATGGCAGCCGGCAGTGTGACCGGGAATATG ACTGCAAGGACATGAGCGATGAAGTTGGCTGCGTTAATGGTG AGCGCTGGCCATCTGGTTTTCCATCCCCATTCTCTGT ACAGAGAATGGGGGATGGAAAACCAGATGGCCAGCGCTCAC CATTAAACGCAGCCAACTTCATCGCTCATGTCTTGCAGTCATA TTCCCGGTCACACTGCCGGCTGCCATGGATGCAGTTT	3789
	ATGAGCGATGAAGTTGG	3790
	CCAACTTCATCGCTCAT	3791
		3792
Hypercholesterolaemia Cys249Tyr TGC-TAC	ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGGCC ATCTGGTTTTCCATCCCCATTCTCTGTGCCTTGCTGCT AGCAGCAAGGCACAGAGAATGGGGGATGGAAAACCAGATGG CCAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCATGTC CTTGCAAGTCATATTCCCGGTCACACTGCCGGCTGCCAT AGTTGGCTGCGTTAATG	3793
		3794

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATTAACGCAGCCAACT	3795
Hypercholesterolaemia Glu256Lys cGAG-AAG	AGGCTCAGACACACCTGACCTTCCTCCTTCCTCTCTCTGGCT CTCACAGTGACACTCTGCAGGGGACCCAACAAGTTCAAGTGT CACAGCGGCGAATGCATCACCTGGACAAAGTCTGCA	3796
	TGCAGACTTTGTCCAGGGTGTGATTGCGCGCTGTGACACT TGAAGTTGTTGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCA GAGAGAGGAAGGAGGAAGGTCAGGTGTGTCTGAGCCT	3797
	CACTCTGCGAGGGACCC	3798
	GGGTCCCTCGCAGAGTG	3799
Hypercholesterolaemia Ser265Arg AGCg-AGA	CCTCTCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAA CAAGTTCAAGTGTACAGCGGCGAATGCATCACCTGGACAA AGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCA	3800
	TGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTC CAGGGTGTGATTGCGCGCTGTGACACTTGAAGTTGTTGGG TCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGAGAGG	3801
	TGTCACAGCGGCGAATG	3802
	CATTCGCGCTGTGACA	3803
Hypercholesterolaemia Glu267Lys cGAA-AAA	TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTACAGCGGCGAATGCATCACCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG	3804
	CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCCAGGGTGTGATTGCGCGCTGTGACACTTGAAGTTGT TGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGA	3805
	ACAGCGGCGAATGCATC	3806
	GATGCATTGCGCGCTGT	3807
Hypercholesterolaemia Glu267Ter cGAA-TAA	TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTACAGCGGCGAATGCATCACCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG	3808
	CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCCAGGGTGTGATTGCGCGCTGTGACACTTGAAGTTGT TGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGA	3809
	ACAGCGGCGAATGCATC	3810
	GATGCATTGCGCGCTGT	3811
Hypercholesterolaemia Lys273Glu cAAA-GAA	ACACTCTGCGAGGGGACCCAACAAGTTCAAGTGTACAGCGG CGAATGCATCACCTGGACAAAGTCTGCAACATGGCTAGAGA CTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCG	3812
	CGCACTCTTTGATGGGTTTCTGACCAAGTCCCGGCAGTCTC TAGCCATGTTGCAGACTTGTGTCAGGGTGTGATTGCGCGC TGTGACACTTGAAGTTGTTGGGTCCCTCGCAGAGTGT	3813
	CCCTGGACAAAGTCTGC	3814
	GCAGACTTTGTCCAGGG	3815
Hypercholesterolaemia Cys275Ter TGCg-TGA	CGAGGGACCCAACAAGTTCAAGTGTACAGCGGCGAATGCA TCACCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGG GACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCT	3816

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGACTCACC G CACTCTTTGATGGGTTCACTGACCAGTCCCG GCAGTCTCTAGCCATGTTG <u>C</u> AGACTTTGTCCAGGGTGATGCA TTCGCCGCTGTGACACTTGA <u>A</u> CTTGTGGGTCCCTCG	3817
	AAAGTCTGCAACATGGC	3818
	GCCATGTTGCAGACTTT	3819
		3820
Hypercholesterolaemia Asp280Gly GAC-GGC	AGTTCAAGTGTACAGCGGCGAATGCATCACCCTGGACAAAG TCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAA CCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCT	3821
	AGCCGCCTGCACCGAGACTCACC G CACTCTTTGATGGGTTCA TCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTG TCCAGGGTGATGCATTGCGCCGCTGTGACACTTGA <u>A</u> CT	3822
	GGCTAGAGACTGCCGGG	3823
	CCCGGCAGTCTCTAGCC	3824
Hypercholesterolaemia Cys281Tyr TGC-TAC	TCAAGTGTACAGCGGCGAATGCATCACCCTGGACAAAGTCT GCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCC ATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGC	3825
	GCAAGCCGCCTGCACCGAGACTCACC G CACTCTTTGATGGG TTCATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGAC TTTGTCCAGGGTGATGCATTGCGCCGCTGTGACACTTGA	3826
	TAGAGACTGCCGGGACT	3827
	AGTCCCGGCAGTCTCTA	3828
Hypercholesterolaemia Asp283Asn gGAC-AAC	TGTCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAAC ATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAA GAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT	3829
	ACTCTGCAAGCCGCCTGCACCGAGACTCACC G CACTCTTTGA TGGGTTCACTGACCAGTCCCGGCAGTCTCTAGCCATGTTGC AGACTTTGTCCAGGGTGATGCATTGCGCCGCTGTGACA	3830
	ACTGCCGGGACTGGTCA	3831
	TGACCAGTCCCGGCAGT	3832
Hypercholesterolaemia Asp283Glu GACT-GAG	TCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACAT GGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAG AGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTT	3833
	AAACTCTGCAAGCCGCCTGCACCGAGACTCACC G CACTCTTT GATGGGTTCACTGACCAGTCCCGGCAGTCTCTAGCCATGTT GCAGACTTTGTCCAGGGTGATGCATTGCGCCGCTGTGA	3834
	TGCCGGGACTGGTCAGA	3835
	TCTGACCAGTCCCGGCA	3836
Hypercholesterolaemia Asp283Tyr gGAC-TAC	TGTCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAAC ATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAA GAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT	3837
	ACTCTGCAAGCCGCCTGCACCGAGACTCACC G CACTCTTTGA TGGGTTCACTGACCAGTCCCGGCAGTCTCTAGCCATGTTGC AGACTTTGTCCAGGGTGATGCATTGCGCCGCTGTGACA	3838
	ACTGCCGGGACTGGTCA	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGACCAGTCCC GG CAGT	3839
Hypercholesterolaemia Trp284Term TGGt-TGA	CAGCGGCGAATGCATCACCTGGACAAAGTCTGCAACATGG CTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGT GCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTG	3840
	CACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACT CTTTGATGGGTTCATCTGAC CAGTCCC GG CAGTCTCTAGCCA TGTTGCAGACTTTGTCCAGGGTGATGCATTGCGCGCTG	3841
	CGGGACTGGTCAGATGA	3842
	TCATCTGACCA TCCCCG	3843
	GCGGCGAATGCATCACCTGGACAAAGTCTGCAACATGGCTA GAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGC GGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGG	3844
Hypercholesterolaemia Ser285Leu TCA-TTA	CCCACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCA CTCTTTGATGGGTTCATCTGACCAGTCCC GG CAGTCTCTAGC CATGTTGCAGACTTTGTCCAGGGTGATGCATTGCGCGC	3845
	GGA CTGGTCAGATGAAC	3846
	GTT CATCTGACCAGTCC	3847
	CCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGAC TGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTG CAGGCGGCTTGCAGAGTTTGTGGGGAGCCAGGAAAGGGA	3848
Hypercholesterolaemia Lys290Arg AAA-AGA	TCCCTTTCTGGCTCCCCACAAACTCTGCAAGCCGCCTGCAC CGAGACTCACCGCACTCTTTGATGGGTTCATCTGACCAGTCC CGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGG	3849
	ACCCATCAAAGAGTGCG	3850
	CGCACTCTTTGATGGGT	3851
	GGGTAGGGGCCCCGAGAGTGACCAGTCTGCATCCCCTGGCCC TGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTG TTCCACAGTCTGCAATGACCTTAAGATCGGCTACGAGTG	3852
Hypercholesterolaemia Cys297Phe TGC-TTC	CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAG CCGCCGTTGTTGTCCAAGCATTGTTGGTCCCTGCGCAGGG CCAGGGGATGCAGACTGGTCACTCTCGGGCCCCTACCC	3853
	CAACGAATGCTTGGACA	3854
	TGTCCAAGCATTGTTG	3855
	GGGTAGGGGCCCCGAGAGTGACCAGTCTGCATCCCCTGGCCC TGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTG TTCCACAGTCTGCAATGACCTTAAGATCGGCTACGAGTG	3856
Hypercholesterolaemia Cys297Tyr TGC-TAC	CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAG CCGCCGTTGTTGTCCAAGCATTGTTGGTCCCTGCGCAGGG CCAGGGGATGCAGACTGGTCACTCTCGGGCCCCTACCC	3857
	CAACGAATGCTTGGACA	3858
	TGTCCAAGCATTGTTG	3859
	TGCATCCCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGA CAACAACGGCGGCTGTTCC CAGTCTGCAATGACCTTAAGAT CGGCTACGAGTGCTGTGCCCCGACGGCTTCCAGCTGG	3860

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATC TTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCC AAGCATTCTGTTGGTCCCTGCGCAGGGCCAGGGGATGCA GCTGTTCCACGTCTGC	3861
	GCAGACGTGGGAACAGC	3862
		3863
Hypercholesterolaemia Cys308Gly cTGC-GGC	CCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAA CGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTA CGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCC	3864
	GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGT TGTGTCCAAGCATTCTGTTGGTCCCTGCGCAGGGCCAGGG CCCACGTCTGCAATGAC	3865
	GTCATTGCAGACGTGGG	3866
		3867
		3868
Hypercholesterolaemia Cys308Tyr TGC-TAC	CCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAAC GGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCA TGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGT GTTGTCCAAGCATTCTGTTGGTCCCTGCGCAGGGCCAGG CCACGTCTGCAATGACC	3869
	GGTCATTGCAGACGTGG	3870
		3871
		3872
		3873
Hypercholesterolaemia Gly314Ser cGGC-AGC	ACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCT TGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC GGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTG CACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCG GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGAC GTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCTGTTGGT TTAAGATCGGCTACGAG	3874
	CTCGTAGCCGATCTTAA	3875
		3876
		3877
		3878
Hypercholesterolaemia Gly314Val GGC-GTC	CCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCT GCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC GGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGA TCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTC GGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGA CGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCTGTTGG TAAGATCGGCTACGAGT	3879
	ACTCGTAGCCGATCTTA	3880
		3881
		3882
		3882
Hypercholesterolaemia Tyr315Term TACg-TAA	CGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAA TGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTT CCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTC GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCA GACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCTG ATCGGCTACGAGTGCCT	3882

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGCACTCGTAGCCGAT	3883
Hypercholesterolaemia Cys317Gly gTGC-GGC	TGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGAC CTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCA GCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCGGG	3884
	CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGG AAGCCGTGCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTC ATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA	3885
	GCTACGAGTGCCTGTGC	3886
	GCACAGGCACTCGTAGC	3887
Hypercholesterolaemia Cys317Ser gTGC-AGC	TGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGAC CTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCA GCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCGGG	3888
	CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGG AAGCCGTGCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTC ATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA	3889
	GCTACGAGTGCCTGTGC	3890
	GCACAGGCACTCGTAGC	3891
Hypercholesterolaemia Pro320Arg CCC-CGC	ACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCG GCTACGAGTGCCTGTGCCCGACGGCTTCCAGCTGGTGGCC CAGCGAAGATGCGAAGGTGATTTCGGGTGGGACTGAG	3892
	CTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCC ACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGAT CTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGT	3893
	CCTGTGCCCGACGGCT	3894
	AGCCGTCGGGGCACAGG	3895
Hypercholesterolaemia Asp321Asn cGAC-AAC	AACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGC TACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCA GCGAAGATGCGAAGGTGATTTCGGGTGGGACTGAGCC	3896
	GGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGG CCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCG ATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTT	3897
	TGTGCCCCGACGGCTTC	3898
	GAAGCCGTCGGGGCACA	3899
Hypercholesterolaemia Asp321Glu GACg-GAG	CGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTA CGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGC GAAGATGCGAAGGTGATTTCGGGTGGGACTGAGCCCT	3900
	AGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTG GGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAG CCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCG	3901
	TGCCCCGACGGCTTCCA	3902
	TGGAAGCCGTCGGGGCA	3903
Hypercholesterolaemia Gly322Ser cGGC-AGC	GGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCG AAGATGCGAAGGTGATTTCGGGTGGGACTGAGCCCTG	3904

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGGGCTCAGTCCCACCCGGAATCACCTTCGCATCTTCGCT GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCC	3905
	GCCCCGACGGCTTCCAG	3906
	CTGGAAGCCGTCGGGGC	3907
Hypercholesterolaemia Gln324Term cCAG-TAG	TGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGC CTGTGCCCCGACGGCTTCCAGCTGGTGGCCAGCGAAGATG CGAAGGTGATTTCCGGGTGGGACTGAGCCCTGGGCCCC	3908
	GGGGCCAGGGCTCAGTCCCACCCGGAATCACCTTCGCAT CTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCA CTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACA	3909
	ACGGCTTCCAGCTGGTG	3910
	CACCAGCTGGAAGCCGT	3911
Hypercholesterolaemia Arg329Pro CGA-CCA	ATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGC TTCCAGCTGGTGGCCAGCGAAGATGCGAAGGTGATTTCCG GGTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGAC	3912
	GTCAGGAAGCGCAGAGGGGGCCAGGGCTCAGTCCCACCC GGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAG CCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCAT	3913
	GGCCCAGCGAAGATGCG	3914
	CGCATCTTCGCTGGGCC	3915
Hypercholesterolaemia Arg329Term gCGA-TGA	AATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGG CTTCCAGCTGGTGGCCAGCGAAGATGCGAAGGTGATTTCC GGGTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGA	3916
	TCAGGAAGCGCAGAGGGGGCCAGGGCTCAGTCCCACCCG GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATT	3917
	TGGCCCAGCGAAGATGC	3918
	GCATCTTCGCTGGGCCA	3919
Hypercholesterolaemia Glu336Lys tGAG-AAG	TCTAGCCATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTC TCTCTTCAGATATCGATGAGTGTGAGGATCCCGACACCTGC AGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGT	3920
	ACTTGTAGCCACCCTCCAGGTTACGCAGAGCTGGCTGCAG GTGTCGGGATCCTGACACTCATCGATATCTGGAAGAGAGAGA AAGAGGCTTGGTGGGGAGGCTCTTCCCCAATGGCTAGA	3921
	ATATCGATGAGTGTGAG	3922
	CTGACACTCATCGATAT	3923
Hypercholesterolaemia Gln338Term tCAG-TAG	CATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTCTCTCTT CCAGATATCGATGAGTGTGAGGATCCCGACACCTGCAGCCAG CTCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGT	3924
	ACTGGCACTTGTAGCCACCCTCCAGGTTACGCAGAGCTGG CTGCAGGTGTCGGGATCCTGACACTCATCGATATCTGGAAGA GAGAGAAAGAGGCTTGGTGGGGAGGCTCTTCCCCAATG	3925
	ATGAGTGTGAGGATCCC	3926

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGGATCCTGACACTCAT	3927
Hypercholesterolaemia Cys343Arg cTGC-CGC	TCCCCACCAAGCCTCTTTCTCTCTTCCAGATATCGATGAGT GTCAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTG GAGGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCC	3928
	GGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCCAGGT TCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTGACACTCA TCGATATCTGGAAGAGAGAGAAAGAGGCTTGGTGGGGA	3929
	CCGACACCTGCAGCCAG	3930
	CTGGCTGCAGGTGTCGG	3931
Hypercholesterolaemia Gln345Arg CAG-CGG	CAAGCCTCTTTCTCTCTGTTCCAGATATCGATGAGTGTGAGGA TCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTG GCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGA	3932
	TCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCC TCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG ACACTCATCGATATCTGGAAGAGAGAGAAAGAGGCTTG	3933
	CTGCAGCCAGCTCTGCG	3934
	CGCAGAGCTGGCTGCAG	3935
Hypercholesterolaemia Cys347Tyr TGC-TAC	TCTTTCTCTCTTCCAGATATCGATGAGTGTGAGGATCCCGA CACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACA AGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCA	3936
	TGGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTGTA GCCACCCTCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGG GATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGA	3937
	CCAGCTCTGCGTGAACC	3938
	GGTTCACGCAGAGCTGG	3939
Hypercholesterolaemia Cys347Arg cTGC-CGC	CTCTTTCTCTCTTCCAGATATCGATGAGTGTGAGGATCCCG ACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTAC AAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCC	3940
	GGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAG CCACCCTCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGG ATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGAG	3941
	GCCAGCTCTGCGTGAAC	3942
	GTTACGCAGAGCTGGC	3943
Hypercholesterolaemia Gly352Asp GGT-GAT	CAGATATCGATGAGTGTGAGGATCCCGACACCTGCAGCCAGC TCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAG GAAGGCTTCCAGCTGGACCCCCACACGAAGGCCTGCAA	3944
	TTGCAGGCCTTCGTGTGGGGGTCCAGCTGGAAGCCTTCCTC ACACTGGCACTTGTAGCCACCCTCCAGGTTACGCAGAGCTG GCTGCAGGTGTCGGGATCCTGACACTCATCGATATCTG	3945
	CCTGGAGGGTGGCTACA	3946
	TGTAGCCACCCTCCAGG	3947
Hypercholesterolaemia Tyr354Cys TAC-TGC	TCGATGAGTGTGAGGATCCCGACACCTGCAGCCAGCTCTGC GTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAGGAAGG CTTCCAGCTGGACCCCCACACGAAGGCCTGCAAGGCTGT	3948

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ACAGCCTTGCAGGCCTTCGTGTGGGGGTCCAGCTGGAAGCC TTCCTCACACTGGCACTTGTAGCCACCCTCCAGGTTACGCA GAGCTGGCTGCAGGTGTCGGGATCCTGACACTCATCGA GGGTGGCTACAAGTGCC	3949
	GGCACTTGTAGCCACCC	3950
		3951
		3952
Hypercholesterolaemia Cys358Arg gTGT-CGT	CAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGA GGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGG ACCCCCACACGAAGGCCTGCAAGGCTGTGGGTGAGCACG CGTGCTCACCCACAGCCTTGCAGGCCTTCGTGTGGGGGTCC AGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCC AGGTTACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG AGTGCCAGTGTGAGGAA	3953
	TTCCTCACACTGGCACT	3954
		3955
		3956
Hypercholesterolaemia Gln363Term cCAG-TAG	TGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGTG CCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCACACGAAGG CCTGCAAGGCTGTGGGTGAGCACGGGAAGGCGGCGGGTG CACCCGCCGCTTCCCGTGCTCACCCACAGCCTTGCAGGCC TTCGTGTGGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCA CTTGTAGCCACCCTCCAGGTTACGCAGAGCTGGCTGCA AAGGCTTCCAGCTGGAC	3957
	GTCCAGCTGGAAGCCTT	3958
		3959

EXAMPLE 22**UDP-glucuronosyltransferase - UGT1**

Mutations in the human UGT1 gene result in a range of disease syndromes, ranging from relatively common diseases such as Gilbert's syndrome, which effects up to 7% of the population, to rare disorders such as Crigler-Najjar syndrome. Symptoms of these diseases are the result of diminished bilirubin conjugation and typically present with jaundice or, when mild, as an incidental finding during routing laboratory analysis. Severe cases of Crigler-Najjar syndrome are caused by an absence of UGT1 activity and the majority of these patients die in the neonatal period. The only known treatment is liver transplant. The attached table discloses the correcting oligonucleotide base sequences for the UGT1 oligonucleotides of the invention.

Table 29
UGT1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Crigler-Najjar syndrome 2 Leu15Arg CTG-CGG	GCAGGAGCAAAGGCGCCATGGCTGTGGAGTCCCAGGGCGG ACGCCCACCTTGTCTGGGCTGCTGCTGTGTGCTGGGCC CAGTGGTGTCCCATGCTGGGAAGATACTGTTGATCCCAGT	3960
	ACTGGGATCAACAGTATCTTCCCAGCATGGGACACCACTGGG CCCAGCACACACAGCAGCAGGCCAGGACAAGTGGGCGTCC GCCCTGGGACTCCACAGCCATGGCGCCTTTGCTCCTGC	3961
	CCTGGGCCCTGCTGCTGT	3962
	ACAGCAGCAGGCCCAGG	3963
Crigler-Najjar syndrome 1 Gln49Term CAG-TAG	GGGAAGATACTGTTGATCCCAGTGGATGGCAGCCACTGGCT GAGCATGCTTGGGGCCATCCAGCAGCTGCAGCAGAGGGGAC ATGAAATAGTTGTCCTAGCACCTGACGCCTCGTTGTACA	3964
	TGTACAACGAGGCGTCAGGTGCTAGGACAACATTTTCATGTC CCCTCTGCTGCAGCTGCTGGATGGCCCCAAGCATGCTCAGC CAGTGGCTGCCATCCACTGGGATCAACAGTATCTTCCC	3965
	GGGCCATCCAGCAGCTG	3966
	CAGCTGCTGGATGGCCC	3967
Crigler-Najjar syndrome 1 Gly71Arg GGA-AGA	CAGCAGAGGGGACATGAAATAGTTGTCCTAGCACCTGACGCC TCGTTGTACATCAGAGACGGAGCATTTTACACCTTGAAGACGT ACCCTGTGCCATTCCAAAGGGAGGATGTGAAAGAGT	3968
	ACTCTTTCACATCCTCCCTTTGGAATGGCAGAGGGTACGTCTT CAAGGTGTAAAATGCTCCGTCTCTGATGTACAACGAGGCGTC AGGTGCTAGGACAACATTTTCATCTCCCCTCTGCTG	3969
	TCAGAGACGGAGCATTT	3970
	AAATGCTCCGTCTCTGA	3971
Gilbert syndrome Pro229Gln CCG-CAG	GGGTGAAGAACATGCTCATTGCCTTTTCACAGAACTTTCTGTG CGACGTGGTTTATTCCCCGTATGCAACCCTTGCCTCAGAATT CCTTCAGAGAGAGGTGACTGTCCAGGACCTATTGAG	3972
	CTCAATAGGTCCTGGACAGTCACCTCTCTCTGAAGGAATTCT GAGGCAAGGGTTGCATACGGGGAATAAACCACGTCGCACAG AAAGTTCTGTGAAAAGGCAATGAGCATGTTCTTCACCC	3973
	TTATTCCCCGTATGCAA	3974
	TTGCATACGGGGAATAA	3975
Crigler-Najjar syndrome 1 Cys280Term TGC-TGA	TGTGAAGGATTACCCTAGGCCCATCATGCCCAATATGGTTTTT GTTGGTGAATCAACTGCCTTCACCAAAATCCACTATCCCAG GTGTGTATTGGAGTGGGACTTTTACATGCGTATATT	3976
	AATATACGCATGTAAAAGTCCCACTCCAATACACACCTGGGAT AGTGGATTTTGGTGAAGGCAGTTGATTCCACCAACAAAAACC ATATTGGGCATGATGGGCCTAGGGTAATCCTTCACA	3977

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ATCAACTGCCTTCACCA	3978
	TGGTGAAGGCAGTTGAT	3979
Crigler-Najjar syndrome 1 Ala292Val GCC-GTC	ATCAAAGAATATGAGAAAAATTAAGTGAATTTTTCTTCTGG CTCTAGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATG GAATTGTGGTTTTCTCTTTGGGATCAATGGTCTC	3980
	GAGACCATTGATCCCAAAGAGAAAACCACAATTCCATGTTCTC CAGAAGCATTAAATGTAGGCTTCAAATTCCTAGAGCCAGAAGAA AAATTTTCAGTTAATTTTTCTCATATTCTTTGAT	3981
	ATTTGAAGCCTACATTA	3982
	TAATGTAGGCTTCAAAT	3983
Crigler-Najjar syndrome 1 Gly308Glu GGA-GAA	AGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATGGAAT TGTGGTTTTCTCTTTGGGATCAATGGTCTCAGAAATTCCAGAG AAGAAAGCTATGGCAATTGCTGATGCTTTGGGCAA	3984
	TTGCCCAAAGCATCAGCAATTGCCATAGCTTTCTTCTCTGGAA TTTCTGAGACCATTGATCCCAAAGAGAAAACCACAATTCCATG TTCTCCAGAAGCATTAAATGTAGGCTTCAAATTCCT	3985
	CTCTTTGGGATCAATGG	3986
	CCATTGATCCCAAAGAG	3987
Crigler-Najjar syndrome 1 Gln331Term CAG-TAG	GTCTCAGAAATTCAGAGAAGAAAGCTATGGCAATTGCTGAT GCTTTGGGCAAATCCCTCAGACAGTAAGAAGATTCTATACCA TGGCCTCATATCTATTTTACAGGAGCGCTAATCCC	3988
	GGGATTAGCGCTCCTGTGAAAATAGATATGAGGCCATGGTAT AGAATCTTCTTACTGTCTGAGGGATTTTGCCCAAAGCATCAGC AATTGCCATAGCTTTCTTCTCTGGAATTTCTGAGAC	3989
	AAATCCCTCAGACAGTA	3990
	TACTGTCTGAGGGATTT	3991
Crigler-Najjar syndrome 1 Trp335Term TGG-TGA	TCTAATCATATTATGTTCTTTCTTTACGTTCTGCTCTTTTGCC CCTCCCAGGTCCTGTGGCGGTACACTGGAACCCGACCATCG AATCTTGCGAACAACACGATACTTGTTAAGTGGCTA	3992
	TAGCCACTTAACAAGTATCGTGTTGTTGCAAGATTCGATGGT CGGGTTCCAGTGTACCGCCACAGGACCTGGGAGGGGGCAAAA AGAGCAGAACGTAAAGAAAGAACATAATATGATTAGA	3993
	GTCCTGTGGCGGTACAC	3994
	GTGTACCGCCACAGGAC	3995
Crigler-Najjar syndrome 1 Gln357Arg CAA-CGA	ACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATAC TTGTAAAGTGGCTACCCCAAACGATCTGCTTGGTATGTTGG GCGGATTGGATGTATAGGTCAAACCAGGGTCAAATTA	3996
	TAATTTGACCCTGGTTTGACCTATACATCCAATCCCTCCCAACA TACCAAGCAGATCGTTTTGGGGTAGCCACTTAACAAGTATCGT GTTGTTGCAAGATTGATGGTCGGGTTCCAGTGT	3997

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCTACCCC <u>A</u> AAACGATC	3998
	GATCGTTTT <u>G</u> GGGTAGC	3999
Crigler-Najjar syndrome 1 Gln357Term CAA-TAA	TACACTGGAACCCGACCATCGAATCTTGCGAACAAACACGATACTTGTTAAGTGGCTACCC <u>C</u> AAAACGATCTGCTTGGTATGTTGGCGGATTGGATGTATAGGTCAAACCAGGGTCAAATT	4000
	AATTTGACCCTGGTTTGACCTATACATCCAATCCGCCCAACATACCAAGCAGATCGTTTT <u>G</u> GGGTAGCCACTTAACAAGTATCGTGTGTTGCGAAGATTCGATGGTCGGGTTCCAGTGTA	4001
	GGCTACCCC <u>A</u> AAACGAT	4002
	ATCGTTTT <u>G</u> GGGTAGCC	4003
Gilbert syndrome Arg367Gly CGT-GGT	AACTCAGAGATGTAAGTCTGACATCCTCCCTATTTGCATCTCAGGTCACCCGATGACCC <u>G</u> TGCCTTTATCACCCATGCTGGTTC	4004
	GAACGCCATTGCATATGCTTTCATAAACACCATGGGAACCAGCATGGGTGATAAAGGCAC <u>G</u> GGTCATCGGGTGACCTGAGATGCAAAATAGGGAGGATGTCAGCAGTTACATCTCTGAGTT	4005
	CGATGACCC <u>G</u> TGCCTTT	4006
	AAAGGCAC <u>G</u> GGTCATCG	4007
Crigler-Najjar syndrome 1 Ala368Thr GCC-ACC	TCAGAGATGTAAGTCTGACATCCTCCCTATTTGCATCTCAGGTCACCCGATGACCC <u>G</u> TGCCTTTATCACCCATGCTGGTTC	4008
	ATGGTGTTTATGAAAGCATATGCAATG <u>G</u> CGTTCCCA	
	TGGGAACGCCATTGCATATGCTTTCATACACCATGGGAAC CAGCATGGGTGATAAAGGCACGGGTGATCGGGTGACCTGAGATGCAAAATAGGGAGGATGTCAGCAGTTACATCTCTGA	4009
	TGACCCGT <u>G</u> CCTTTATC	4010
	GATAAAGGCACGGGTCA	4011
Crigler-Najjar syndrome 1 Ser375Phe TCC-TTC	CCTCCCTATTTTGCATCTCAGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTCCCATGGTGTTTATGAAAGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTTTGG	4012
	CCAAACAAGGGCATCATCACCATGGGAACGCCATTGCATATGCTTTCATAAACACCATGGGAACCAGCATGGGTGATAAAGGCA CGGGTCATCGGGTGACCTGAGATGCAAAATAGGGAGG	4013
	TGCTGGTTCCCATGGTG	4014
	CACCATGGGAACCAGCA	4015
Crigler-Najjar syndrome 1 Ser381Arg AGC-AGG	AGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTC CATGGTGTTTATGAAAGCATATGCAATGGCGTTCCCATGGT GATGATGCCCTTGTTTGGTGATCAGATGGACAATGCA	4016
	TGCATTGTCCATCTGATCACCACAAAGGGCATCATCACCATGGGAACGCCATTGCATATGCTTTCATAAACACCATGGGAACC AGCATGGGTGATAAAGGCACGGGTGATCGGGTGACCT	4017

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATGAAAGCATATGCAA	4018
	TTGCATATGCTTTCATA	4019
Crigler-Najjar syndrome 1 Ala401Pro GCA-CCA	AGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTTT GGTGATCAGATGGACAATGCAAAGCGCATGGAGACTAAGGG AGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTG	4020
	CAGAAGTCATTTCCAGAACATTCAGGGTCACTCCAGCTCCCT TAGTCTCCATGCGCTTTGATTGTCCATCTGATCACCAAACAA GGGCATCATCACCATGGGAACGCCATTGCATATGCT	4021
	TGGACAATGCAAAGCGC	4022
	GCGCTTTGATTGTCCA	4023
	GGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTGAA GATTTAGAAAATGCTCTAAAGCAGTCATCAATGACAAAAGGT AAGAAAGAAGATACAGAAGAATACTTTGGTCATGGC	4024
	GCCATGACCAAAGTATTCTTCTGTATCTTCTTTCTTACCTTTTG TCATTGATGACTGCTTTTAGAGCATTTTCTAAATCTTCAGAAGT CATTTCCAGAACATTCAGGGTCACTCCAGCTCC	4025
Crigler-Najjar syndrome 1 Lys428Glu AAA-GAA	ATGCTCTAAAGCAGTC	4026
	GACTGCTTTTAGAGCAT	4027
Crigler-Najjar syndrome 1 Tyr486Asp TAC-GAC	ATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGCAGCCC ACGACCTCACCTGGTACCAGTACCATTCTTGGACGTGATTG GTTTCCTCTTGGCCGTCGTGCTGACAGTGGCCTTCATCA	4028
	TGATGAAGGCCACTGTCAGCACGACGGCCAAGAGGAAACCA ATCACGTCCAAGGAATGGTACTGGTACCAGGTGAGGTCGTG GGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGTGCCTCAT	4029
	GGTACCAGTACCATTCC	4030
	GGAATGGTACTGGTACC	4031
	ACAAGGGCGCGCCACACCTGCGCCCCGCAGCCCACGACCT CACCTGGTACCAGTACCATTCTTGGACGTGATTGGTTTCCT CTTGGCCGTCGTGCTGACAGTGGCCTTCATCACCTTTAA	4032
Crigler-Najjar syndrome 1 Ser488Phe TCC-TTC	TTAAAGGTGATGAAGGCCACTGTCAGCACGACGGCCAAGAG GAAACCAATCACGTCCAAGGAATGGTACTGGTACCAGGTGAG GTCGTGGGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGT	4033
	GTACCATTCTTGGACG	4034
	CGTCCAAGGAATGGTAC	4035

EXAMPLE 23**Alzheimer's Disease - Amyloid precursor protein (APP)**

Over the past few decades Alzheimer's disease (AD), once considered a rare disorder, has become recognized as a major public health problem. Although there is no agreement on the exact prevalence of Alzheimer's disease, in part due to difficulties of diagnosis, studies consistently point to an exponential rise in prevalence of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest tasks. Anatomic changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and internal neurofibrillary tangles.

At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with a particular allele of APOE (see Example 20); AD3 is caused by mutation in a gene encoding a 7-transmembrane domain protein, presenilin-1 (PSEN1), and AD4 is caused by mutation in a gene that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2). The attached table discloses the correcting oligonucleotide base sequences for the APP oligonucleotides of the invention.

Table 30
APP Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Glu665Asp GAG-GAC	CTGCATACTTTAATTATGATGTAATACAGGTTCTGGGTTGACA AATATCAAGACGGAGGAGATCTCTGAAGTGAAGATGGATGCA GAATTCCGACATGACTCAGGATATGAAGTTCATCAT	4036
	ATGATGAACTTCATATCCTGAGTCATGTCGGAATTCTGCATCC ATCTTCACTTCAGAGATCTCCTCCGTCTTGATATTTGTCAACC CAGAACCTGTATTACATCATAATTAAAGTATGCAG	4037
	ACGGAGGAGATCTCTGA	4038
	TCAGAGATCTCCTCCGT	4039
Alzheimer disease Ala692Gly GCA-GGA	ATTATATTGCATTTAGAAATTAATTCCTTTTCTTAATTTGTTTT CAAGGTGTTCTTTGCAGAAAGATGTGGGTTCAAACAAAGGTGC AATCATTGGAATCATGGTGGGCGGTGTTGTCAT	4040

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTTTG TTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAATT AAGAAAAAGAATTTTAATTTCTAAATGCAATATAAT	4041
	GTTCTTTGCAGAAGATG	4042
	CATCTTCTGCAAAGAAC	4043
Alzheimer disease Glu693Gln GAA-CAA	TATATTGCATTTAGAAATTAAAATTCTTTTCTTAATTTGTTTC AAGGTGTTCTTTGCAGAAGATGTGGGTTCAAACAAAGGTGCA ATCATTGGACTCATGGTGGGCGGTGTTGTCATAG	4044
	CTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTT TGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAA TTAAGAAAAAGAATTTTAATTTCTAAATGCAATATA	4045
	TCTTTGCAGAAGATGTG	4046
	CACATCTTCTGCAAAGA	4047
Alzheimer disease Glu693Gly GAA-GGA	ATATTGCATTTAGAAATTAAAATTCTTTTCTTAATTTGTTTCA AGGTGTTCTTTGCAGAAGATGTGGGTTCAAACAAAGGTGCAA TCATTGGACTCATGGTGGGCGGTGTTGTCATAGC	4048
	GCTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCT TTGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAA ATTAAGAAAAAGAATTTTAATTTCTAAATGCAATAT	4049
	CTTTGCAGAAGATGTGG	4050
	CCACATCTTCTGCAAAG	4051
Alzheimer disease Ala713Thr GCG-ACG	GAAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATG GTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTG GTGATGCTGAAGAAGAAACAGTACACATCCATTCATC	4052
	GATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGT GATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAG TCCAATGATTGCACCTTTGTTTGAACCCACATCTTC	4053
	TTGTCATAGCGACAGTG	4054
	CACTGTCGCTATGACAA	4055
Schizophrenia Ala713Val GCG-GTG	AAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGG TGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGG TGATGCTGAAGAAGAAACAGTACACATCCATTCATCA	4056
	TGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGG TGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGA GTCCAATGATTGCACCTTTGTTTGAACCCACATCTT	4057
	TGTCATAGCGACAGTGA	4058
	TCACTGTCGCTATGACA	4059
Alzheimer disease Val715Met GTG-ATG	GTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGC GGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATG CTGAAGAAGAAACAGTACACATCCATTCATCATGGTG	4060
	CACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCAC CAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCAC CATGAGTCCAATGATTGCACCTTTGTTTGAACCCAC	4061
	TAGCGACAGTGATCGTC	4062

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GACGATCACTGTCGCTA	4063
Alzheimer disease Ile716Val ATC-GTC	GGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGT GTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTG AAGAAGAAACAGTACACATCCATTCATCATGGTGTGG	4064
	CCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCAT CACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCC CACCATGAGTCCAATGATTGCACCTTTGTTTGAACC	4065
	CGACAGTGATCGTCATC	4066
	GATGACGATCACTGTCG	4067
Alzheimer disease Val717Gly GTC-GGC	CAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTG TCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGA AGAAACAGTACACATCCATTCATCATGGTGTGGTGA	4068
	TCCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCA GCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACAC CGCCCACCATGAGTCCAATGATTGCACCTTTGTTTG	4069
	AGTGATCGTCATCACCT	4070
	AGGTGATGACGATCACT	4071
Alzheimer disease Val717Ile GTC-ATC	TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTT GTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAG AAGAAACAGTACACATCCATTCATCATGGTGTGGTGG	4072
	CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAG CATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACC GCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA	4073
	CAGTGATCGTCATCACC	4074
	GGTGATGACGATCACTG	4075
Alzheimer disease Val717Phe GTC-TTC	TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTT GTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAG AAGAAACAGTACACATCCATTCATCATGGTGTGGTGG	4076
	CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAG CATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACC GCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA	4077
	CAGTGATCGTCATCACC	4078
	GGTGATGACGATCACTG	4079
Alzheimer disease Leu723Pro CTG-CCG	TTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCG TCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCAT TCATCATGGTGTGGTGGAGGTAGGTAAACTTGACTG	4080
	CAGTCAAGTTTACCTACCTCCACCACACCATGATGAATGGAT GTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCA CTGTCGCTATGACAACACCGCCCACCATGAGTCCAA	4081
	GGTGATGCTGAAGAAGA	4082
	TCTTCTTCAGCATCACC	4083

EXAMPLE 24
Alzheimer's Disease - presenilin-1 (PSEN1)

The attached table discloses the correcting oligonucleotide base sequences for the PSEN1 oligonucleotides of the invention.

Table 31
PSEN1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
Alzheimer disease Ala79Val GCC-GTC	CCCGGCAGGTGGTGGAGCAAGATGAGGAAGAAGATGAGGAG CTGACATTGAAATATGGCGCCAAGCATGTGATCATGCTCTTTG TCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC	4084
	GTAGCCACGACCACCACCATGCAGAGAGTCACAGGGACAAA GAGCATGATCACATGCTTGGCGCCATATTTCAATGTCAGCTC CTCATCTTCTTCCTCATCTTGCTCCACCACCTGCCGGG	4085
	ATATGGCGCCAAGCATG	4086
	CATGCTTGGCGCCATAT	4087
		4088
Alzheimer disease Val82Leu tGTG-CTG	GTGGTGGAGCAAGATGAGGAAGAAGATGAGGAGCTGACATT GAAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGT GACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAAGT	4089
	ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCACATGCTTGGCGCCATATTTCAATG TCAGCTCCTCATCTTCTTCCTCATCTTGCTCCACCAC	4090
	CCAAGCATGTGATCATG	4091
	CATGATCACATGCTTGG	4092
		4093
Alzheimer disease Val96Phe gGTC-TTC	AAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGTG ACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAAGTCAGTC AGCTTTTATACCCGGAAGGATGGGCAGCTGTACGTAT	4094
	ATACGTACAGCTGCCCATCCTTCCGGGTATAAAAGCTGACTG ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCACATGCTTGGCGCCATATTT	4095
	TGGTGGTGGTCGTGGCT	4096
	AGCCACGACCACCACCA	4097
		4098
Alzheimer disease Phe105Leu TTTt-TTG	CTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC CATTAAAGTCAGTCAGCTTTTATACCCGGAAGGATGGGCAGCT GTACGTATGAGTTTTGTTTTATTATTCTCAAAGCCAG	4099
	CTGGCTTTGAGAATAATAAAACAAACTCATACGTACAGCTGC CCATCCTTCCGGGTATAAAAGCTGACTGACTTAATGGTAGCC ACGACCACCACCATGCAGAGAGTCACAGGGACAAAG	
	GTCAGCTTTTATACCCG	
	CGGGTATAAAAGCTGAC	

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTC	4121
	AAGATACCGAGACTGTG	4122
	CACAGTCTCGGTATCTT	4123
	TATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATA	4124
Alzheimer disease Asn135Asp gAAT-GAT	TATACAGAACCACCAGGAGGATAGTCATGACAACATGACAC	4125
	TGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGTGAATGGGGTATA	4126
	CAATTCTGAATGCTGCC	4127
	GGCAGCATTGAGAATTG	4128
Alzheimer disease Met139Ile ATGa-ATA	AGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTAT	4129
	ATAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACATGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGCCATCATGATCAGTGT	4130
	ACACTGATCATGATGGC	4131
	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4132
Alzheimer disease Met139Lys ATG-AAG	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACATGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGTGCCATCATGATCAGTG	4133
	CACTGATCATGATGGCA	4134
	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4135
	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACATGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGTGCCATCATGATCAGTG	4136
Alzheimer disease Met139Thr ATG-ACG	CACTGATCATGATGGCA	4137
	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4138
	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACATGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGTGCCATCATGATCAGTG	4139
	CACTGATCATGATGGCA	4140
Alzheimer disease Met139Val cATG-GTG	ACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCT	4141
	AGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACATGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGTCTGCCATCATGATCAGT	4142

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGATCATGATGGCAG	4143
Alzheimer disease Ile143Phe cATT-TTT	GAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCT GCCATCATGATCAGTGTCAATTGTTGTCATGACTATCCTCCTGG TGGTTCTGTATAAATACAGGTGCTATAAGGTGAGCA	4144
	TGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGAG GATAGTCATGACAACAATGACACTGATCATGATGGCAGCATTG AGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTC	4145
	TCAGTGTCAATTGTTGTC	4146
	GACAACAATGACACTGA	4147
Alzheimer disease Ile143Thr ATT-ACT	AGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTG CCATCATGATCAGTGTCAATTGTTGTCATGACTATCCTCCTGGT GGTTCTGTATAAATACAGGTGCTATAAGGTGAGCAT	4148
	ATGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGA GGATAGTCATGACAACAATGACACTGATCATGATGGCAGCAT TCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCT	4149
	CAGTGTCAATTGTTGTCA	4150
	TGACAACAATGACACTG	4151
Alzheimer disease Met146Ile ATGa-ATA	CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCAATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA	4152
	TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATG ATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGG	4153
	GTTGTCATGACTATCCT	4154
	AGGATAGTCATGACAAC	4155
Alzheimer disease Met146Ile ATGa-ATC	CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCAATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA	4156
	TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATG ATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGG	4157
	GTTGTCATGACTATCCT	4158
	AGGATAGTCATGACAAC	4159
Alzheimer disease Met146Leu cATG-TTG	GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCAATTGTTGTCATGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA	4160
	TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCATGACAACAATGACACTGATCATGAT GGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCC	4161
	TTGTTGTCATGACTATC	4162
	GATAGTCATGACAACAA	4163
Alzheimer disease Met146Val cATG-GTG	GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCAATTGTTGTCATGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA	4164

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCATGACAACAATGACACTGATCATGAT GGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCC	4165
	TTGTTGTCATGACTATC	4166
	GATAGTCATGACAACAA	4167
	AGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCA GTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAA ATACAGGTGCTATAAGGTGAGCATGAGACACAGATC	4168
Alzheimer disease Thr147Ile ACT-ATT	GATCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACA GAACCACCAGGAGGATAGTCATGACAACAATGACACTGATCA TGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCT	4169
	TGTCATGACTATCCTCC	4170
	GGAGGATAGTCATGACA	4171
	CTTTTAAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTT CTTTTCTAGGTCATCCATGCCTGGCTTATTATATCATCTCTATT GTTGCTGTTCTTTTTTTCATTCATTTACTTGGG	4172
Alzheimer disease His163Arg CAT-CGT	CCCAAGTAAATGAATGAAAAAAGAACAGCAACAATAGAGATG ATATAATAAGCCAGGCATGGATGACCTAGAAAAGAAAGCATT CAATATAATTAACAGGTCCCACAACCCTTAAAAAG	4173
	GGTCATCCATGCCTGGC	4174
	GCCAGGCATGGATGACC	4175
	ACTTTTAAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCTT TCTTTTCTAGGTCATCCATGCCTGGCTTATTATATCATCTCTAT TGTTGCTGTTCTTTTTTTCATTCATTTACTTGG	4176
Alzheimer disease His163Tyr cCAT-TAT	CCAAGTAAATGAATGAAAAAAGAACAGCAACAATAGAGATGA TATAATAAGCCAGGCATGGATGACCTAGAAAAGAAAGCATTTC AATATAATTAACAGGTCCCACAACCCTTAAAAAGT	4177
	AGGTCATCCATGCCTGG	4178
	CCAGGCATGGATGACCT	4179
	AGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTTCTTTTCT AGGTCATCCATGCCTGGCTTATTATATCATCTCTATTGTTGCT GTTCTTTTTTTCATTCATTTACTTGGGGTAAGTT	4180
Alzheimer disease Trp165Cys TGGc-TGC	AACTTACCCCAAGTAAATGAATGAAAAAAGAACAGCAACAAT AGAGATGATATAATAAGCCAGGCATGGATGACCTAGAAAAGA AAGCATTTCATATAATTAACAGGTCCCACAACCCT	4181
	CATGCCTGGCTTATTAT	4182
	ATAATAAGCCAGGCATG	4183
	ACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCAT GCCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTC ATTCATTTACTTGGGGTAAGTTGTGAAATTTT	4184
Alzheimer disease Ser169Leu TCA-TTA	AAAAATTTCACTTACCCCAAGTAAATGAATGAAAAAAGAA CAGCAACAATAGAGATGATATAATAAGCCAGGCATGGATGAC CTAGAAAAGAAAGCATTTCATATAATTAACAGGT	4185
	TATTATATCATCTCTAT	4186

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAGAGATGATATAATA	4187
Alzheimer disease Leu171Pro CTA-CCA	TAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGG CTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATT TACTTGGGGTAAGTTGTGAAATTTTGGTCTG	4188
	CAGACCAAAAATTTCACTTACCCCAAGTAAATGAATGAAA AAAAGAACAGCAACAATAGAGATGATATAATAAGCCAGGCAT GGATGACCTAGAAAAGAAAGCATTTCATATAATTA	4189
	ATCATCTCTATTGTTGC	4190
	GCAACAATAGAGATGAT	4191
Alzheimer disease Leu173Trp TTG-TGG	TATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGGCTTATT ATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTACTTG GGGTAAGTTGTGAAATTTTGGTCTGTCTTTC	4192
	GAAAGACAGACCAAAAATTTCACTTACCCCAAGTAAATGA ATGAAAAAAGAACAGCAACAATAGAGATGATATAATAAGCCA GGCATGGATGACCTAGAAAAGAAAGCATTTCATA	4193
	TCTATTGTTGCTGTTCT	4194
	AGAACAGCAACAATAGA	4195
Alzheimer disease Gly209Arg gGGA-AGA	TATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCT GGAATTTTGGTGTGGTGGGAATGATTTCATTCACTGGAAAG GTCCACTTCGACTCCAGCAGGCATATCTCATTATGA	4196
	TCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTC AGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAG GAGTGCAACAGTAATGTAGTCCACAGCAACGTTATA	4197
	GTGTGGTGGGAATGATT	4198
	AATCATTCCACCACAC	4199
Alzheimer disease Gly209Val GGA-GTA	ATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTG GAATTTTGGTGTGGTGGGAATGATTTCATTCACTGGAAAGGT CCACTTCGACTCCAGCAGGCATATCTCATTATGAT	4200
	ATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTC CAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCA GGAGTGCAACAGTAATGTAGTCCACAGCAACGTTAT	4201
	TGTGGTGGGAATGATT	4202
	AAATCATTCCACCACA	4203
Alzheimer disease Ile213Thr ATT-ACT	TGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGT GGTGGGAATGATTTCATTCACTGGAAGGTCCACTTCGACT CCAGCAGGCATATCTCATTATGATTAGTGCCCTCAT	4204
	ATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGA AGTGGACCTTTCAGTGAATGGAAATCATTCCACCACACCA AAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCA	4205
	GATTTCCATTCACTGGA	4206
	TCCAGTGAATGGAAATC	4207
Alzheimer disease Leu219Pro CTT-CCT	CACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCAT TCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCAT TATGATTAGTGCCCTCATGGCCCTGGTGTATTATCAA	4208

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGA TATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAA ATCATTCCCACCACACCAAATTCCAGATCAGGAGTG AGGTCCACTTCGACTCC	4209
	GGAGTCGAAGTGGACCT	4210
		4211
	ATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCA TATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCA AGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGG	4212
Alzheimer disease Ala231Thr tGCC-ACC	CCAAGATGAGCCACGCAGTCCATTGAGGGAGGTAAGTATGATAA ACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCCT GCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAAT	4213
	TGATTAGTGCCCTCATG	4214
	CATGAGGGCACTAATCA	4215
		4216
Alzheimer disease Ala231Val GCC-GTC	TTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCA ATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAA GTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGC	4217
	GCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTAAGTATGATA AACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCC TGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAA	4218
	GATTAGTGCCCTCATGG	4219
	CCATGAGGGCACTAATC	4220
Alzheimer disease Met233Thr ATG-ACG	TTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCAATCTCA TTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTACCT CCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGAT	4221
	ATCACAGCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTAC TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGA TATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAA	4222
	TGCCCTCATGGCCCTGG	4223
	CCAGGGCCATGAGGGCA	4224
Alzheimer disease Leu235Pro CTG-CCG	GGAAAGGTCCACTTCGACTCCAGCAGGCAATCTCATTATGA TTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTACCTCCCTG AATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAGT	4225
	ACTGAAATCACAGCCAAGATGAGCCACGCAGTCCATTGAGGG AGGTACTTGATAAACACCAGGGCCATGAGGGCACTAATCATA ATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCC	4226
	CATGGCCCTGGTGTTC	4227
	TAAACACCAGGGCCATG	4228
Alzheimer disease Ala246Glu GCG-GAG	TCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTA CCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTC AGTATATGGTAAACCCAAGACTGATAATTTGTTTG	4229
	CAAACAAATTATCAGTCTTGGGTTTTACCATATACTGAAATCAC AGCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTAAGTATGAT AAACACCAGGGCCATGAGGGCACTAATCATAATGA	4230
	ATGGACTGCGTGGCTCA	
		4230

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGAGCCACGCAGTCCAT	4231
Alzheimer disease Leu250Ser TTG-TCG	GTGCCCTCATGGCCCTGGTGTTCATCAAGTACCTCCCTGAAT GGACTGCGTGGCTCATCTGGCTGTGATTCAGTATATGGTA AAACCAAGACTGATAATTTGTTTGTACAGGAATGC	4232
	GCATTCCTGTGACAAACAAATTATCAGTCTTGGGTTTTACCAT ATACTGAAATCACAGCCAAGATGAGCCACGCAGTCCATTCAG GGAGGTACTTGATAAACACCAGGGCCATGAGGGCAC	4233
	GCTCATCTGGCTGTGA	4234
	TCACAGCCAAGATGAGC	4235
Alzheimer disease Ala260Val GCT-GTT	AGTTTAGCCCATACATTTTATTAGATGTCTTTTATGTTTTCTTT TTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCG TATGCTGGTTGAAACAGCTCAGGAGAGAAATGA	4236
	TCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGAC CTTTCGGACACAAAACAGCCACTAAATCTAGAAAAGAAAAAC ATAAAAGACATCTAATAAAATGTATGGGCTAACT	4237
	TTAGTGGCTGTTTTGT	4238
	ACAAAACAGCCACTAAA	4239
Alzheimer disease Leu262Phe TTG-TTC	CCCATACATTTTATTAGATGTCTTTTATGTTTTCTTTTCTAGA TTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTG GTTGAAACAGCTCAGGAGAGAAATGAAACGCTT	4240
	AAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGA AGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAA GAAAACATAAAAGACATCTAATAAAATGTATGGG	4241
	GCTGTTTTGTGTCCGAA	4242
	TTCGGACACAAAACAGC	4243
Alzheimer disease Cys263Arg gTGT-CGT	CCATACATTTTATTAGATGTCTTTTATGTTTTCTTTTCTAGAT TTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTG GTTGAAACAGCTCAGGAGAGAAATGAAACGCTTT	4244
	AAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACG AAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAA AAGAAAACATAAAAGACATCTAATAAAATGTATGG	4245
	CTGTTTTGTGTCCGAAA	4246
	TTTCGGACACAAAACAG	4247
Alzheimer disease Pro264Leu CCG-CTG	ACATTTTATTAGATGTCTTTTATGTTTTCTTTTCTAGATTTAG TGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTG AAACAGCTCAGGAGAGAAATGAAACGCTTTTTCC	4248
	GGAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCA TACGAAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTA GAAAAGAAAACATAAAAGACATCTAATAAAATGT	4249
	TTTGTGTCCGAAAGGTC	4250
	GACCTTTCGGACACAAA	4251
Alzheimer disease Arg269Gly tCGT-GGT	GTCTTTTATGTTTTCTTTTCTAGATTTAGTGGCTGTTTTGTG TCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGA GAGAAATGAAACGCTTTTTCCAGCTCTCATTTACT	4252

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	AGTAAATGAGAGCTGGAAAAGCGTTTCATTTCTCTCCTGAGC TGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAAC AGCCACTAAATCTAGAAAAGAAAACATAAAAGAC GTCCACTTCGTATGCTG	4253
	CAGCATACGAAGTGGAC	4254
		4255
		4256
Alzheimer disease Arg269His CGT-CAT	TCTTTTATGTTTTCTTTTCTAGATTTAGTGGCTGTTTTGTGTC CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGA GAAATGAAACGCTTTTCCAGCTCTCATTTACTC	4257
	GAGTAAATGAGAGCTGGAAAAGCGTTTCATTTCTCTCCTGAG CTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAA CAGCCACTAAATCTAGAAAAGAAAACATAAAAGA TCCACTTCGTATGCTGG	4258
	CCAGCATACGAAGTGGG	4259
		4260
Alzheimer disease Arg278Thr AGA-ACA	TAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGG TTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCT CATTTACTCCTGTAAGTATTTGAGAATGATATTGAA	4261
	TTCAATATCATTCTCAAATACTTACAGGAGTAAATGAGAGCTG GAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCAT ACGAAGTGGACCTTTCGGACACAAAACAGCCACTA TCAGGAGAGAAATGAAA	4262
	TTTCATTTCTCTCCTGA	4263
		4264
Alzheimer disease Glu280Ala GAA-GCA	CTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAAC AGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTAC TCCTGTAAGTATTTGAGAATGATATTGAATTAGTA	4265
	TACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAG AGCTGGAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACC AGCATACGAAGTGGACCTTTCGGACACAAAACAG GAGAAATGAAACGCTTT	4266
	AAAGCGTTTCATTTCTC	4267
		4268
Alzheimer disease Glu280Gly GAA-GGA	CTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAAC AGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTAC TCCTGTAAGTATTTGAGAATGATATTGAATTAGTA	4269
	TACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAG AGCTGGAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACC AGCATACGAAGTGGACCTTTCGGACACAAAACAG GAGAAATGAAACGCTTT	4270
	AAAGCGTTTCATTTCTC	4271
		4272
Alzheimer disease Leu282Arg CTT-CGT	TGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTC AGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTACTCCTG TAAGTATTTGAGAATGATATTGAATTAGTAATCAGT	4273
	ACTGATTACTAATTCAATATCATTCTCAAATACTTACAGGAGTA AATGAGAGCTGGAAAAGCGTTTCATTTCTCTCCTGAGCTGTT TCAACCAGCATACGAAGTGGACCTTTCGGACACA TGAAACGCTTTTCCAG	4274

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGGAAAAAGCGTTTCA	4275
Alzheimer disease Ala285Val GCT-GTT	AAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAA ATGAAACGCTTTTTCCAGCTCTCATTACTCCTGTAAGTATTTG AGAATGATATTGAATTAGTAATCAGTGTAGAATTT	4276
	AAATTCTACACTGATTACTAATTCAATATCATTCTCAAATACTTA CAGGAGTAAATGAGAGCTGGAAAAAGCGTTTCATTCTCTCCT GAGCTGTTTCAACCAGCATACGAAGTGGACCTT	4277
	TTTTCCAGCTCTCATT	4278
	AAATGAGAGCTGGAAAA	4279
Alzheimer disease Leu286Val tCTC-GTC	GGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAAT GAAACGCTTTTTCCAGCTCTCATTACTCCTGTAAGTATTTGA GAATGATATTGAATTAGTAATCAGTGTAGAATTTAT	4280
	ATAAATTCTACACTGATTACTAATTCAATATCATTCTCAAATACT TACAGGAGTAAATGAGAGCTGGAAAAAGCGTTTCATTCTCTC CTGAGCTGTTTCAACCAGCATACGAAGTGGACC	4281
	TTCCAGCTCTCATTAC	4282
	GTAAATGAGAGCTGGAA	4283
Alzheimer disease Gly384Ala GGA-GCA	GTGACCAACTTTTTAATATTTGTAACTTTCTTTTTAGGGGGA GTAAACTTTGGATTGGGAGATTTCATTTTCTACAGTGTCTGG TTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTG	4284
	CAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACA CTGTAGAAAATGAAATCTCCAATCCAAGTTTACTCCCCCTA AAAAGGAAAGGTTACAAATATTAAGTTGGTCAC	4285
	TGGATTGGGAGATTCA	4286
	TGAAATCTCCAATCCA	4287
Alzheimer disease Ser390Ile AGT-ATT	TTTGTAACTTTCTTTTTAGGGGGAGTAAACTTTGGATTGGG AGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCA ACAGCCAGTGGAGACTGGAACACAACCATAGCCTG	4288
	CAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGAG GCTTTACCAACCAGAACTGTAGAAAATGAAATCTCCAATC CAAGTTTACTCCCCCTAAAAGGAAAGGTTACAAA	4289
	TTTCTACAGTGTCTGG	4290
	CCAGAACTGTAGAAA	4291
Alzheimer disease Leu392Val tCTG-GTG	AACCTTTCTTTTTAGGGGGAGTAAACTTTGGATTGGGAGATT TCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACAGC CAGTGGAGACTGGAACACAACCATAGCCTGTTTCG	4292
	CGAAACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTG CTGAGGCTTTACCAACCAGAACTGTAGAAAATGAAATCTCC CAATCCAAGTTTACTCCCCCTAAAAGGAAAGGTT	4293
	ACAGTGTCTGGTTGGT	4294
	ACCAACCAGAACTGT	4295
Alzheimer disease Asn405Ser AAC-AGC	ATTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAAC AGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGC CATATTAATTGTAAGTATACACTAATAAGAATGTGT	4296

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	ACACATTCTTATTAGTGTATACTTACAATTAATATGGCTACGAA ACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGA GGCTTTACCAACCAGAACACTGTAGAAAATGAAAT AGACTGGAACACAACCA	4297
	TGGTTGTGTTCCAGTCT	4298
		4299
		4300
Alzheimer disease Ala409Thr aGCC-ACC	TACAGTGTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGG GACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTG TAAGTATACACTAATAAGAATGTGTCAGAGCTCTTA TAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAATTAAT ATGGCTACGAAACAGGCTATGGTTGTGTTCCAGTCTCCACTG GCTGTTGCTGAGGCTTTACCAACCAGAACACTGTA CAACCATAGCCTGTTTC	4301
	GAAACAGGCTATGGTTG	4302
		4303
		4304
Alzheimer disease Cys410Tyr TGT-TAT	GTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACT GGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGTAAG TATACACTAATAAGAATGTGTCAGAGCTCTTAATGT ACATTAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAAT TAATATGGCTACGAAACAGGCTATGGTTGTGTTCCAGTCTCCA CTGGCTGTTGCTGAGGCTTTACCAACCAGAACAC CATAGCCTGTTTCGTAG	4305
	CTACGAAACAGGCTATG	4306
		4307
		4308
Alzheimer disease Ala426Pro tGCC-CCC	TGTGAATGTGTGCTTTCCCATCTTCTCCACAGGGTTTGTGCC TTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCT CTTCCAATCTCCATCACCTTTGGGCTTGTTTTCT AGAAAACAAGCCCAAAGGTGATGGAGATTGGAAGAGCTGGCA ATGCTTTCTTGAAAATGGCAAGGAGTAATAATGTAAGGCACAA ACCCTGTGGAGAAGATGGGAAAGACACACATTCA TACTCCTTGCCATTTTC	4309
	GAAAATGGCAAGGAGTA	4310
		4311
		4312
Alzheimer disease Pro436Gln CCA-CAA	AGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAA AGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTT TTCTACTTTGCCACAGATTATCTTGTACAGCCTTT AAAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGC CCAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTG AAAATGGCAAGGAGTAATAATGTAAGGCACAAACCCT AGCTCTTCCAATCTCCA	4313
	TGGAGATTGGAAGAGCT	4314
		4315
		4316
Alzheimer disease Pro436Ser tCCA-TCA	CAGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGA AAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTT TTTCTACTTTGCCACAGATTATCTTGTACAGCCTT AAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGCC CAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTGA AAATGGCAAGGAGTAATAATGTAAGGCACAAACCCTG CAGCTCTTCCAATCTCC	4317
		4318

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGAGATTGGAAGAGCTG	4319

EXAMPLE 25**Alzheimer's Disease - presenilin-2 (PSEN2)**

The attached table discloses the correcting oligonucleotide base sequences for the PSEN2 oligonucleotides of the invention.

Table 32**PSEN2 Mutations and Genome-Correcting Oligos**

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Arg62His CGC-CAC	GATGTGGTTTCCCACAGAGAAGCCAGGAGAACGAGGAGGAC GGTGAGGAGGACCCTGACCGCTATGTCTGTAGTGGGGTTCC CGGGCGGCCGCCAGGCCTGGAGGAAGAGCTGACCCTCAA	4320
	TTGAGGGTCAGCTCTTCCTCCAGGCCTGGCGGCCGCCCGGG AACCCCACTACAGACATAGCGGTTCAGGGTCCTCCTCACCGTC CTCCTCGTTCTCCTGGCTTCTCTGTGGGAAACCACATC	4321
	CCCTGACCGCTATGTCT	4322
	AGACATAGCGGTTCAGGG	4323
Alzheimer disease Thr122Pro cACG-CCG	GCCTCGAGGAGCAGTCAGGGCCGGGAGCATCAGCCCTTTGC CTTCTCCCTCAGCATCTACACGACATTCACTGAGGACACACC CTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACA	4324
	TGTTACAGCACGGAGTTGAGGAGGCGCTGGCCCACCGAGGGT GTGTCCTCAGTGAATGTCGTGTAGATGCTGAGGGAGAAGGCA AAGGGCTGATGCTCCCGGCCCTGACTGCTCCTCGAGGC	4325
	GCATCTACACGACATTC	4326
	GAATGTCGTGTAGATGC	4327
Alzheimer disease Asn141Ile AAC-ATC	ACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGCGC CTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTC ATCGTGGTTATGACCATCTTCTTGGTGGTGCTCTACAA	4328
	TTGTAGAGCACCACCAAGAAGATGGTCATAACCACGATGACG CTGATCATGATGAGGGTGTTTCAGCACGGAGTTGAGGAGGCG CTGGCCCACCGAGGGTGTGTCCTCAGTGAATGGCGTGT	4329
	CGTGCTGAACACCCTCA	4330
	TGAGGGTGTTTCAGCACG	4331
Alzheimer disease Met23Valle ATGg-ATA	CCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCA TCATGATCAGTGCGCTCATGGCCCTAGTGTTTCATCAAGTACCT CCCAGAGTGGTCCGCGTGGGTTCATCCTGGGCGCCATC	4332

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO.
	GATGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGT ACTTGATGAACACTAGGGCCATGAGCGCACTGATCATGATGA GGTAGGCCTGCTGCAGCACCAGAGGGCCCTTCCAGTGG GCGCTCATGGCCCTAGT	4333
	ACTAGGGCCATGAGCGC	4334
		4335
	ATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCT CATCATGATCAGTGCGCTCATGGCCCTAGTGTTTCATCAAGTA CCTCCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCA	4336
Alzheimer disease Met239Val cATG-GTG	TGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGTAC TTGATGAACACTAGGGCCATGAGCGCACTGATCATGATGAGG TAGGCCTGCTGCAGCACCAGAGGGCCCTTCCAGTGGAT	4337
	GTGCGCTCATGGCCCTA	4338
	TAGGGCCATGAGCGCAC	4339

EXAMPLE 26 Plant Cells

The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon. Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration(s) of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications within the oligonucleotide, said targeted alteration(s) occurring more frequently than alteration(s) of the genetic sequence by a double-stranded double hairpin chimeric oligonucleotide containing RNA and DNA nucleotides.
2. The oligonucleotide according to claim one that comprises at least one phosphorothioate linkage within the oligonucleotide.
3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.
4. The oligonucleotide according to claim one that comprises a locked nucleotide analog.
5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.
6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.
7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 1-4340.
8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in a subject, comprising administering to the subject an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A non-human organism comprising the cell according to claim 14.

16. A pharmaceutical composition comprising the oligonucleotide according to any one of claims 1 to 7.

17. A method of targeted chromosomal genomic alteration, comprising administering the pharmaceutical composition of claim 16 to a subject.

18. A non-human organism produced by the method of claim 11 or claim 17.

19. A method of optimizing an oligonucleotide for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a

second oligonucleotide, said second oligonucleotide selected from the group of (1) an oligonucleotide that is fully complementary to the target and lacks the mismatch, (2) a fully modified phosphorothiolated oligonucleotide, (3) a fully modified 2'-O-methylated oligonucleotide and (4) a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

20. The method of claim 19 in which the alteration is produced in a cell extract.

21. The method of claim 20 in which the cell extract is selected from the group of a fungal cell extract, a plant cell extract, a rodent cell extract, a primate cell extract and a human cell extract.

22. The method of claim 19 in which the alteration is produced in a cell.

23. The method of claim 21 in which the cell is selected from the group of a fungal cell, a plant cell, a rodent cell, a primate cell and a human cell.

24. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of (1) an oligonucleotide that is fully complementary to the target and lacks the mismatch, (2) a fully modified phosphorothiolated oligonucleotide, (3) a fully modified 2'-O-methylated oligonucleotide and (4) a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

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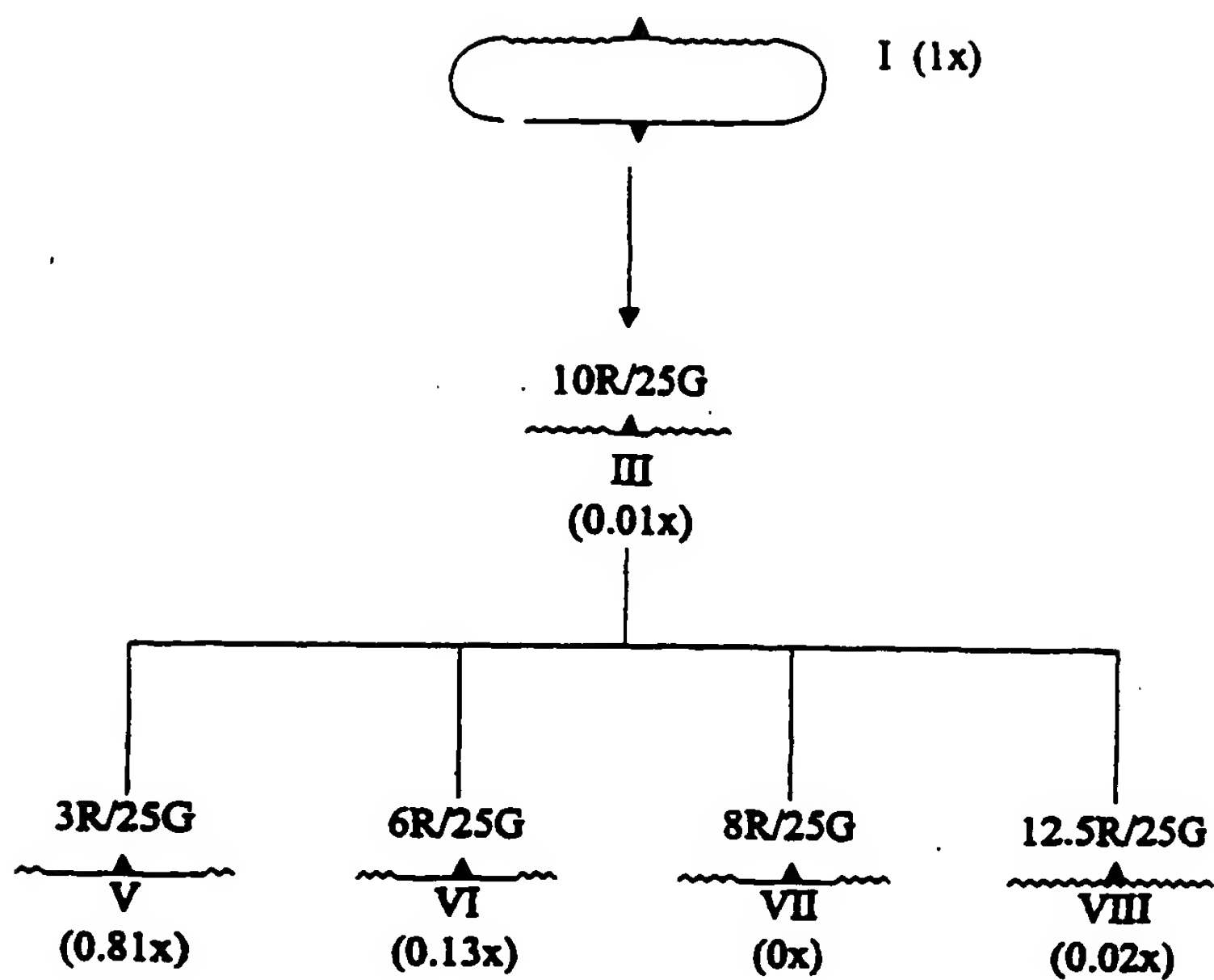


Figure 1A

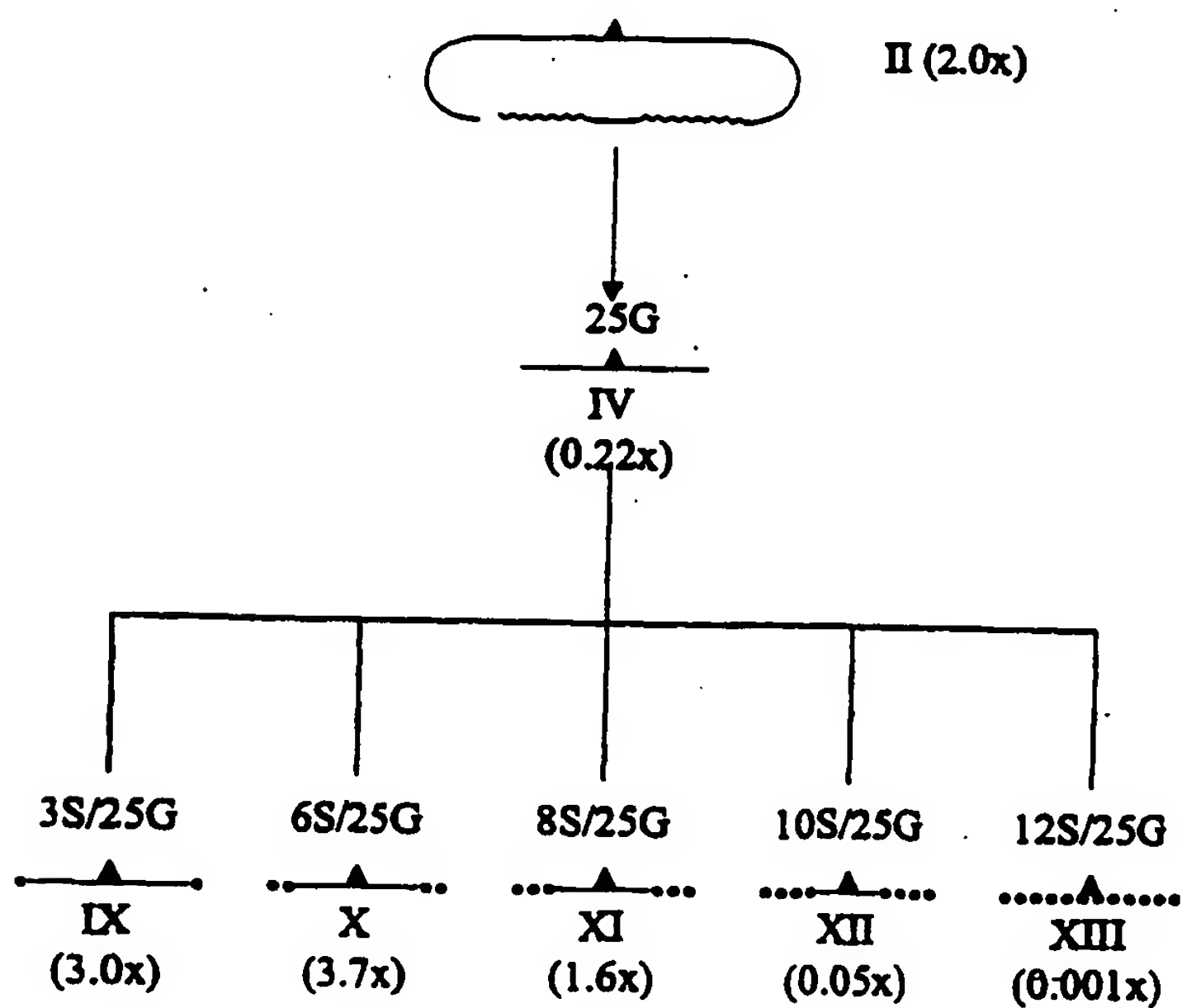
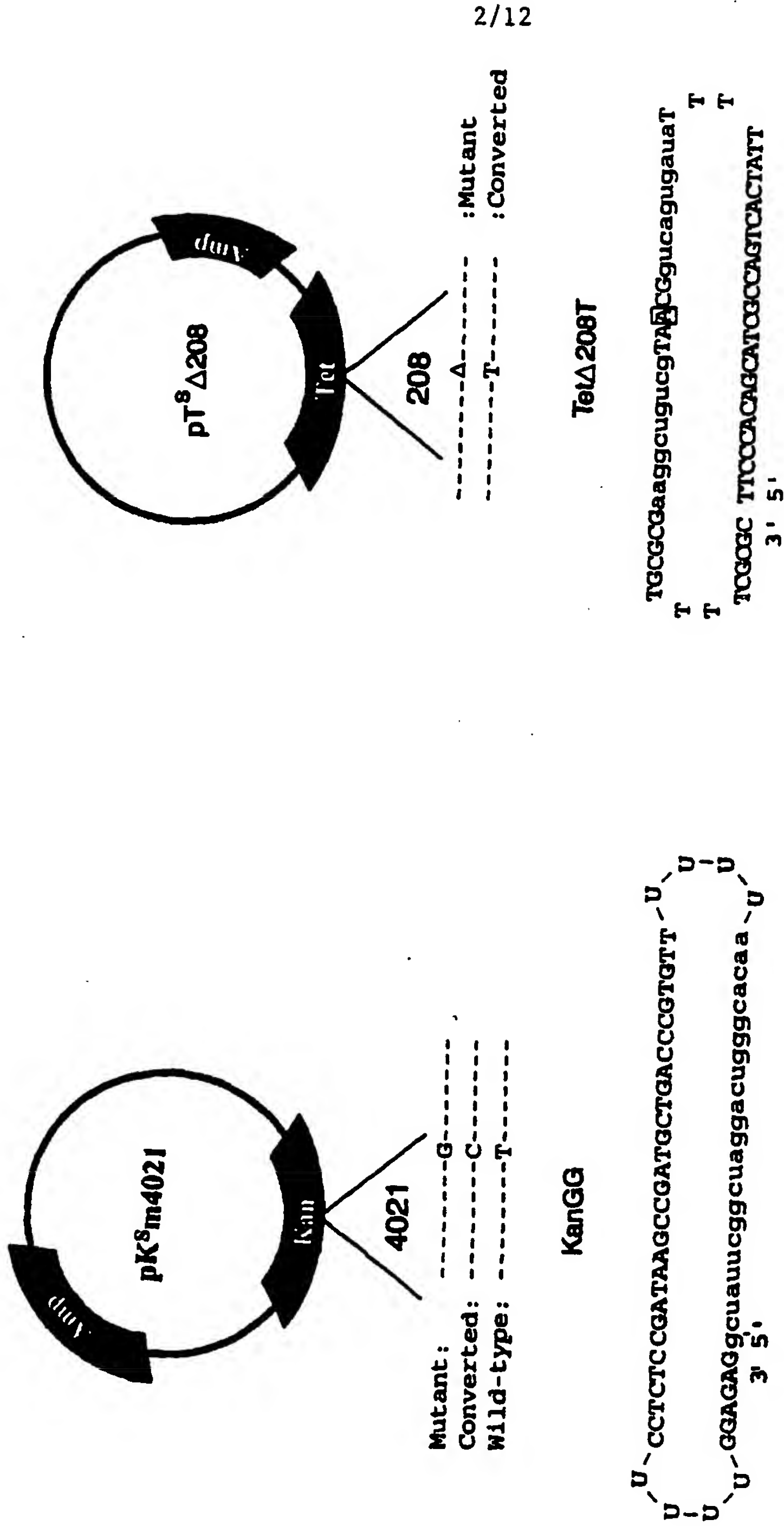


Figure 1B

SUBSTITUTE SHEET (RULE 26)

Plasmids, DNA targets and chimeric oligonucleotides



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Figure 1C

B

TTCGGCTA G GACTGG
AAGCCGAT C CTGACC

Kan mutant sequence

+

U - CCTCTCCGATAAGCCGATGCTGACCCGTGTT - U
U - GGAGAGgcuaauucggcuaggacugggcacaa - U
U - U - U

KanGG chimera

↓

TTCGGCTA C GACTGG
AAGCCGAT G CTGACC

Kan converted sequence

DNA SEQUENCE ANALYSES

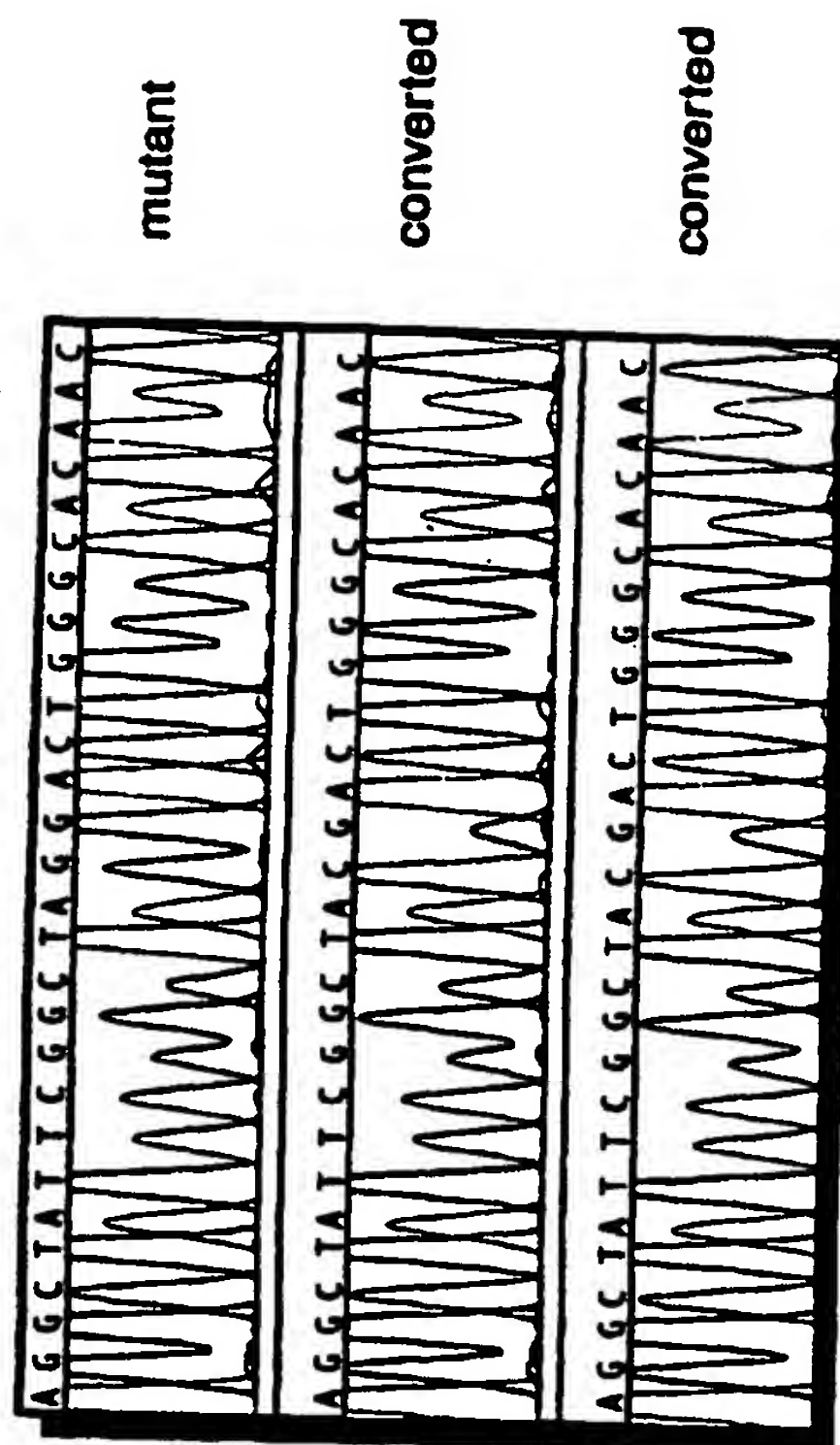


Figure 1D

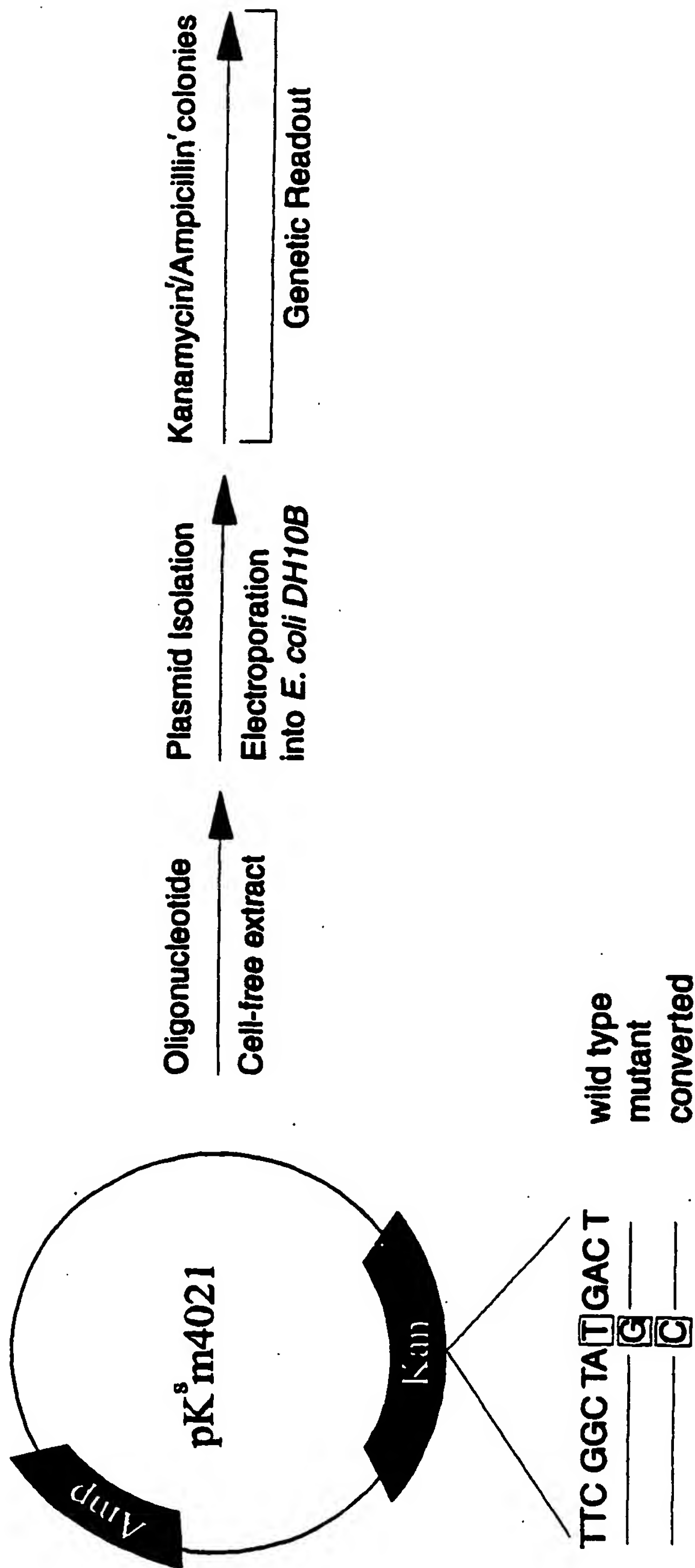
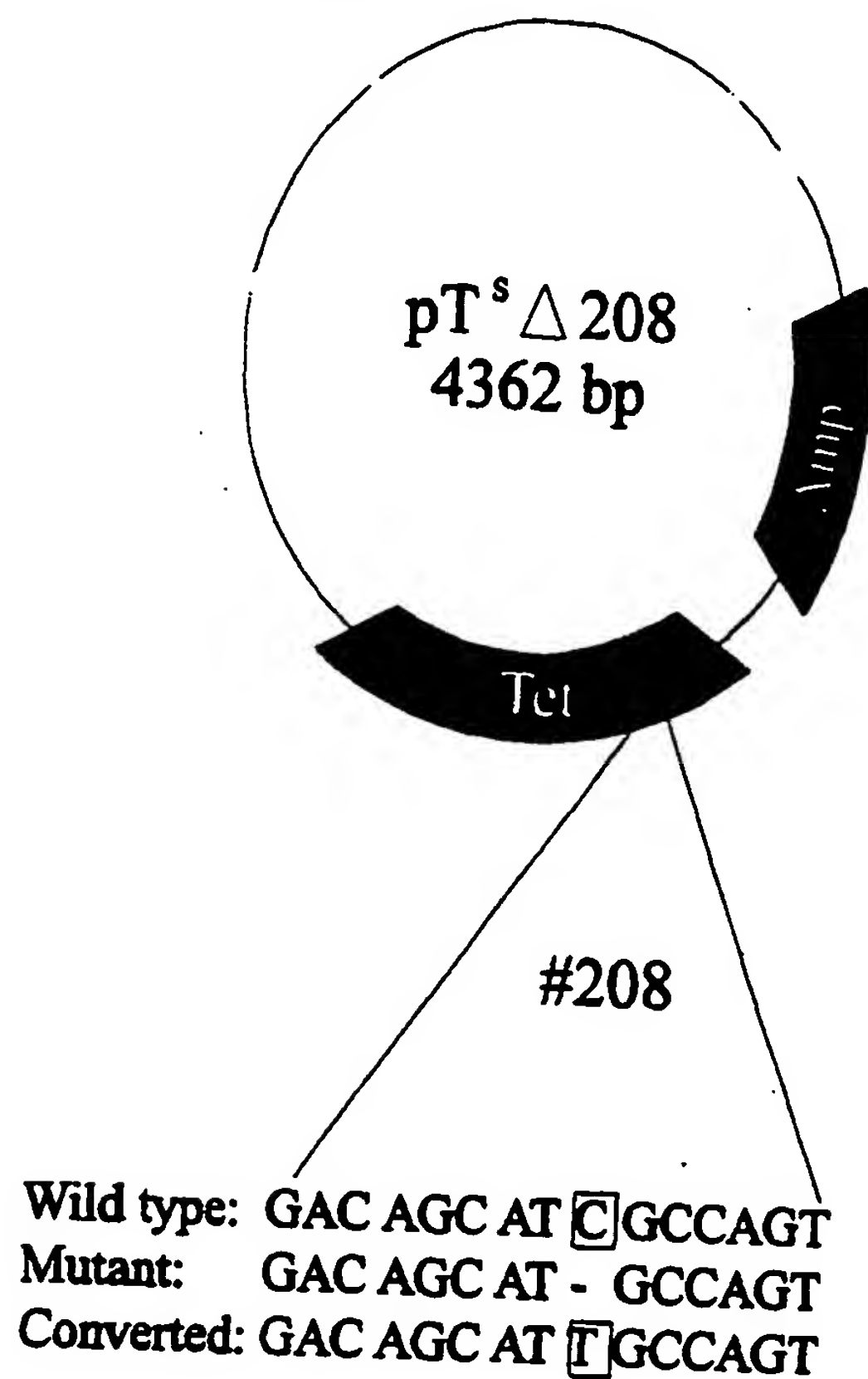


Figure 2

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Sequence analysis of Tet^r plasmid Δ208

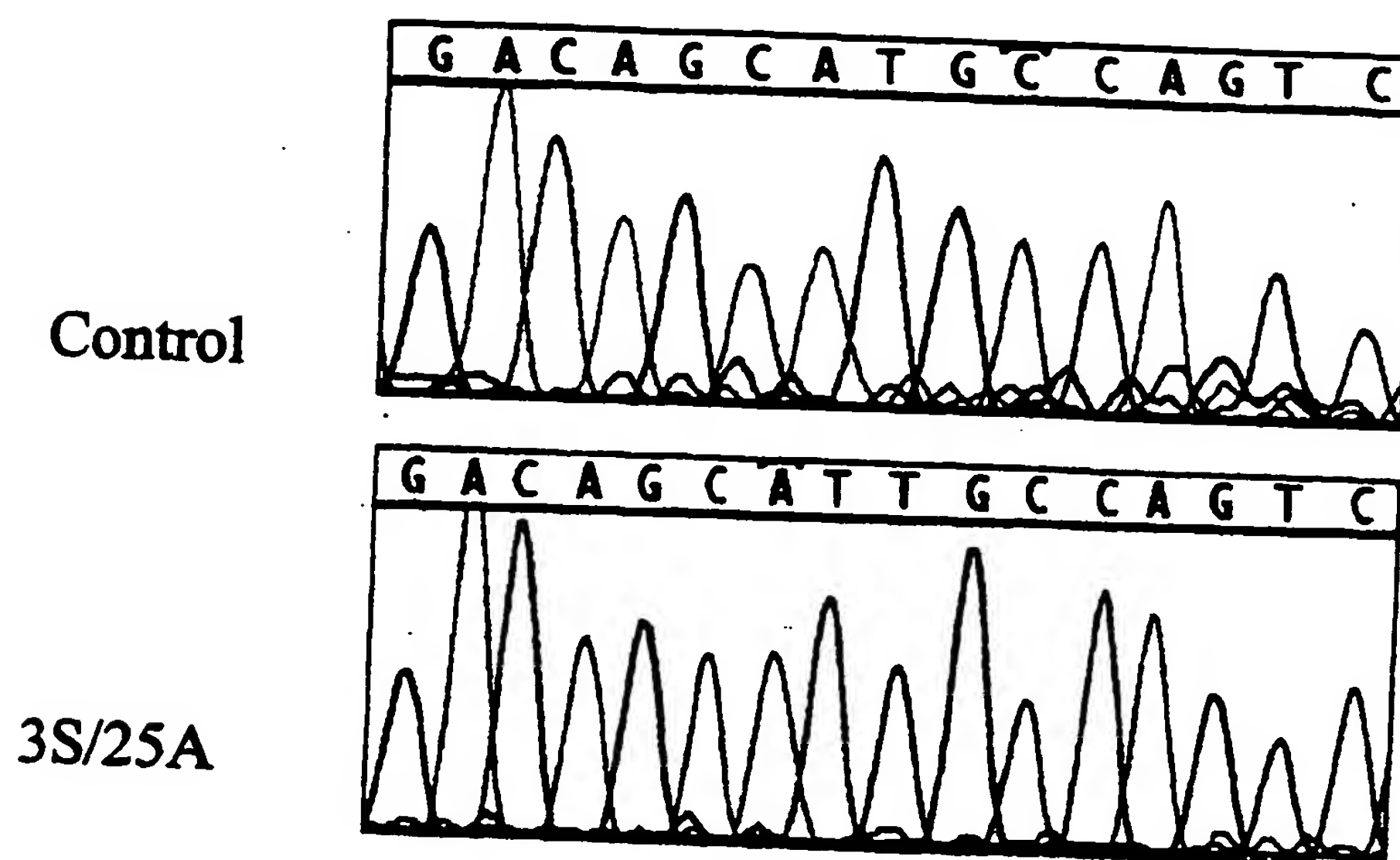


Figure 3

SUBSTITUTE SHEET (RULE 26)

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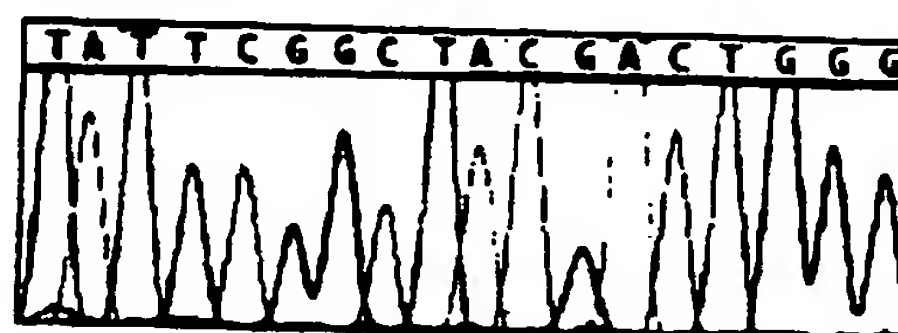
DNA sequence analysis of Kan^r plasmids

Target codon distribution					
oligomer	TAG	TAC	TACTAG	TGG	TCG
1) 3S/25G (20)	—	+	—	—	—
2) 6S/25G (20)	—	+	—	—	—
3) 8S/25G (20)	—	+	—	—	—
4) 10S/25G (18)	—	+	—	—	—
5) 25S/25G (4)	—	—	+(2)	+(2)	—

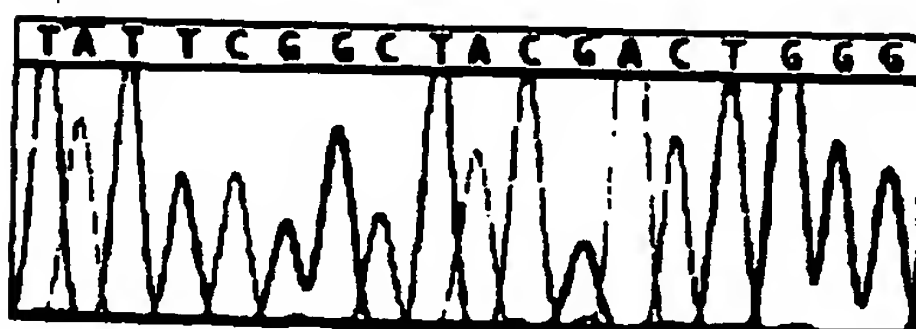
3S/25G



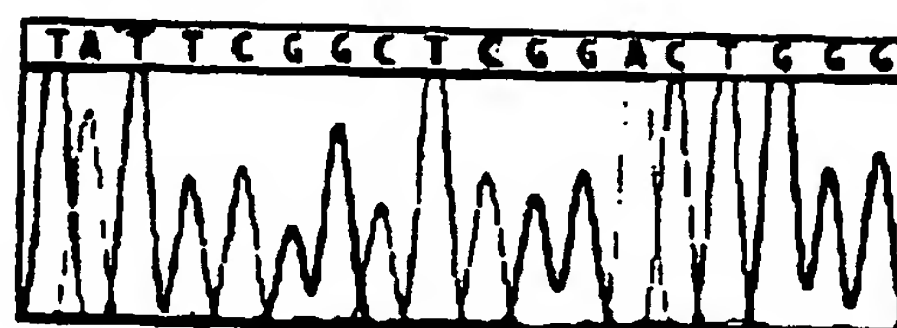
6S/25G



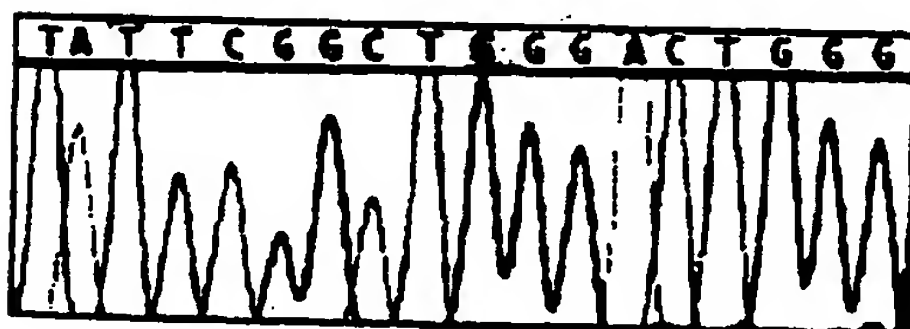
8S/25G



10S/25G



25S/25G



25S/25G

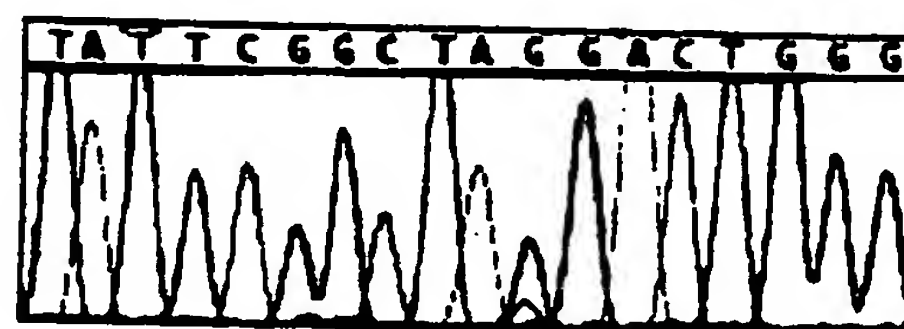


Figure 4

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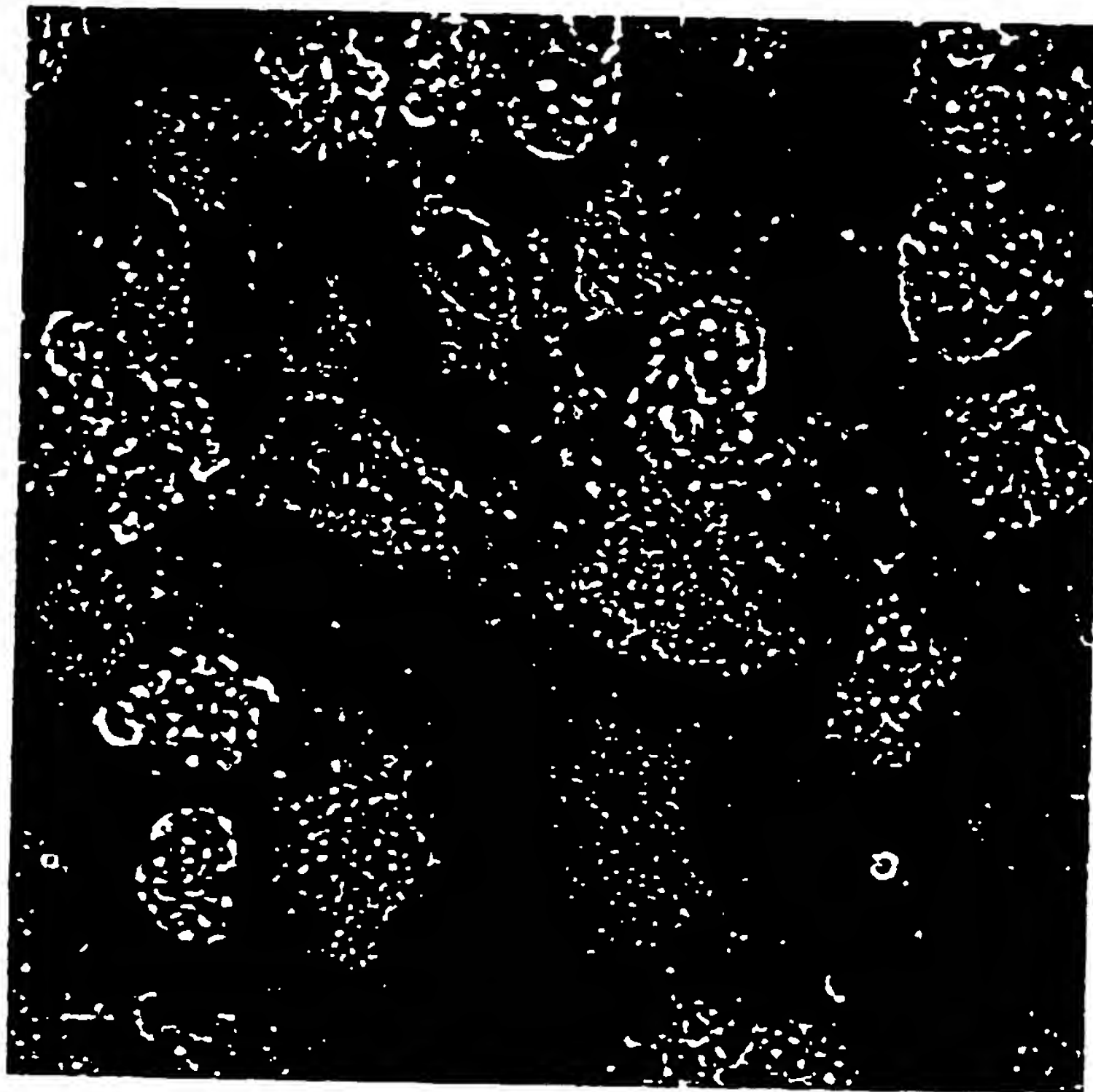


Figure 5

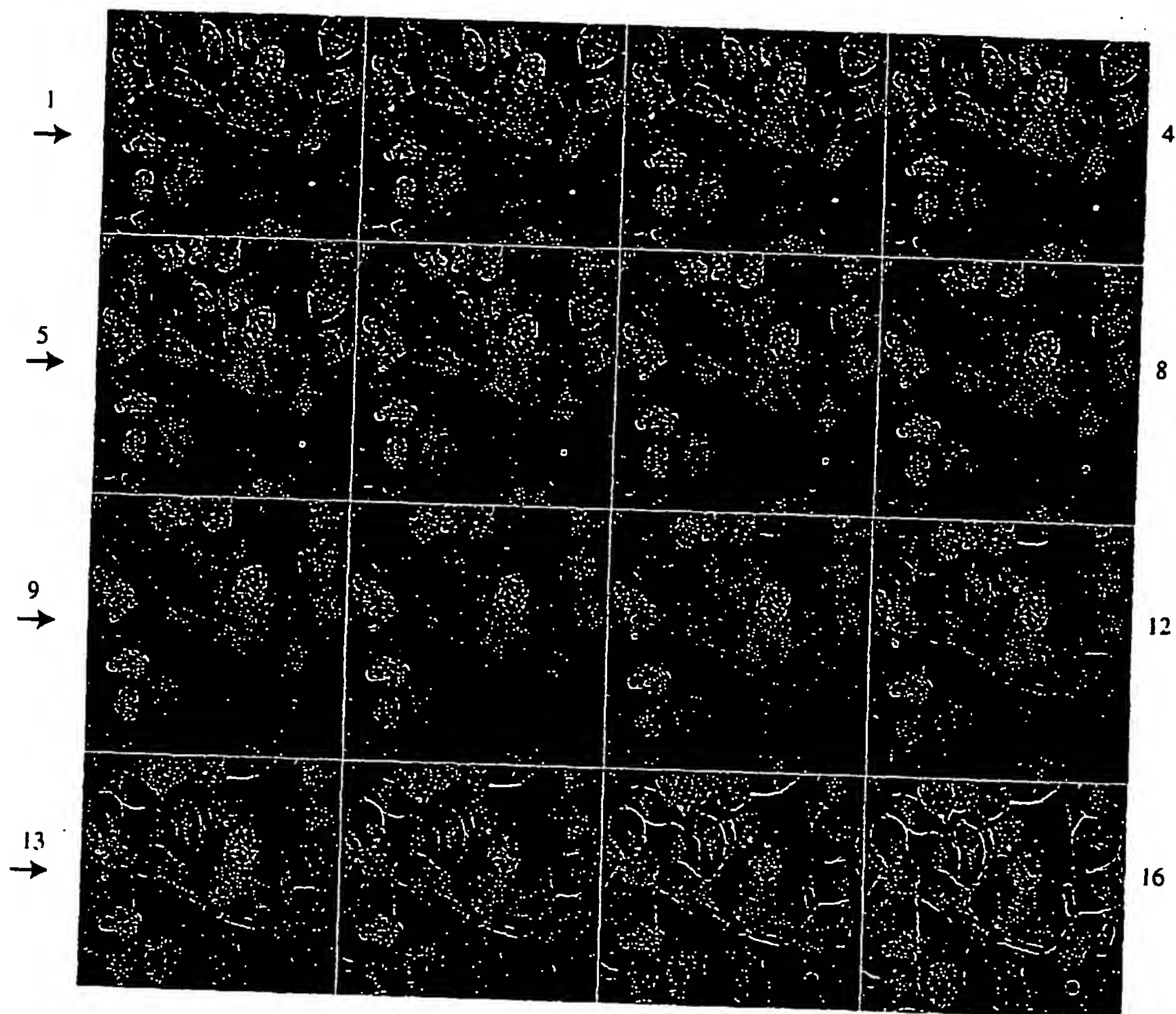
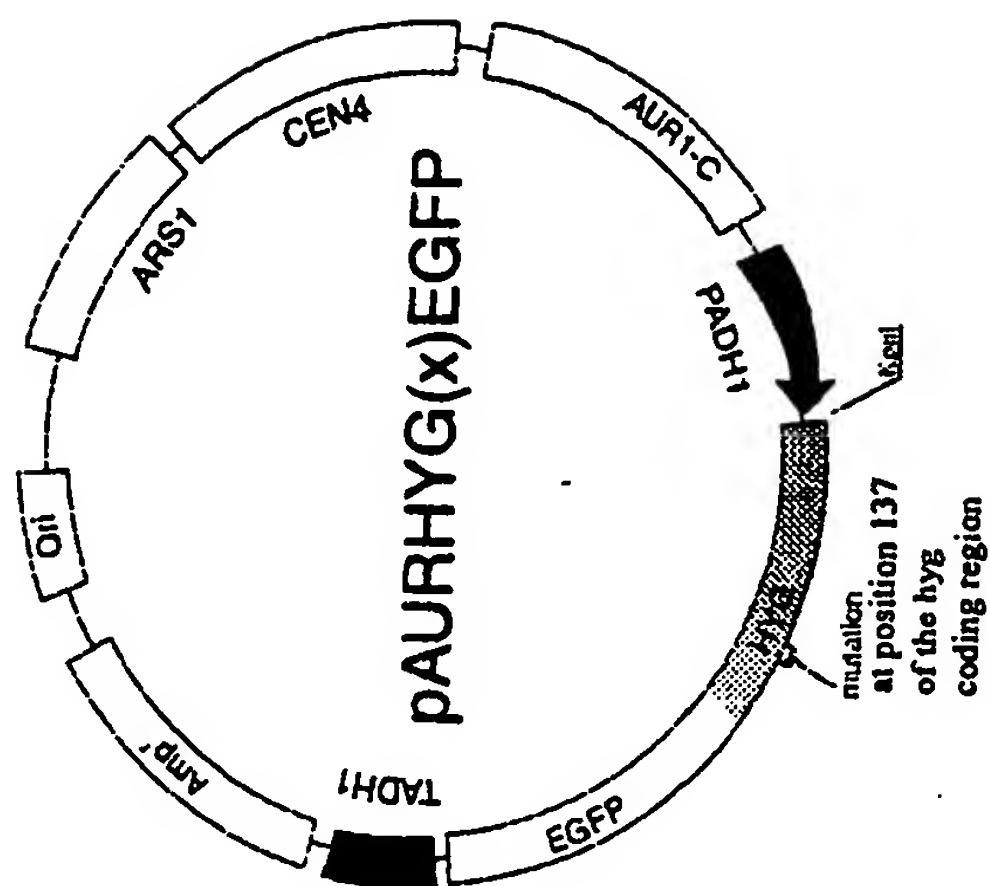


Figure 6

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Sequence of normal allele: GTGGATATGTCCT
 Target/existing mutant: GTGGATAATGTCCT
 Desired alteration: GTGGATACGTCCT

Figure 7A



Sequence of normal allele: GTGGATATGTCCT
 Target/existing mutant: GTGGATAGGTCCT
 Desired alteration: GTGGATACGTCCT

Figure 7B

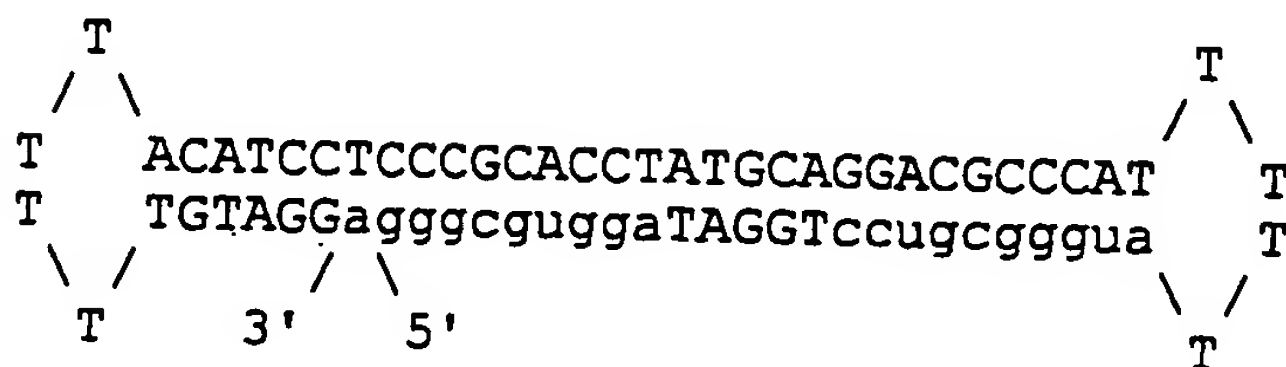
10/12

HvgE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HvgE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC
GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG
CCG ATG GTT TCT AC-3'

HvgE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG
CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA
GCT GAA AGC ACG AG-3'

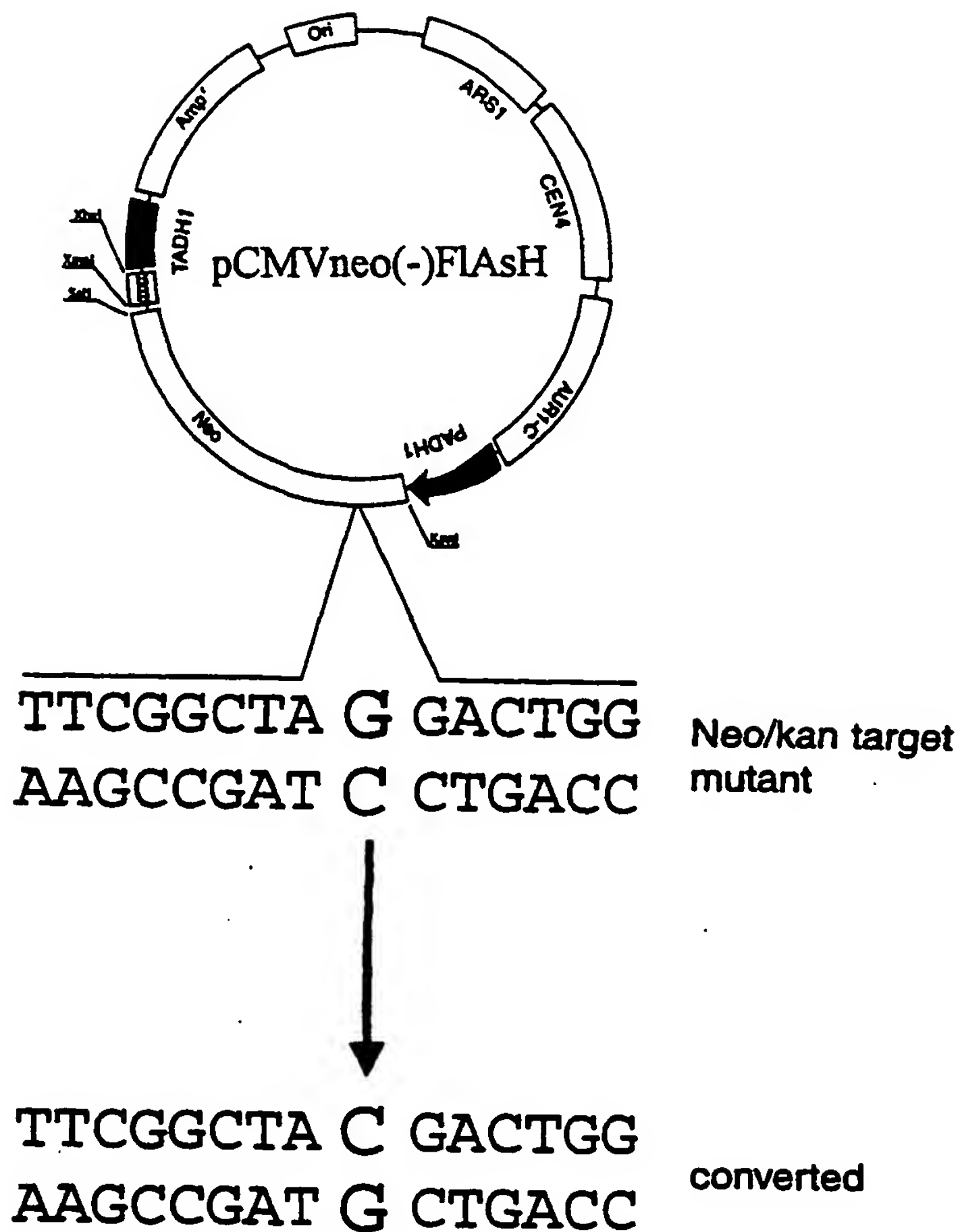
HyqGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT
CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG
A-3'

Figure 8

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FUSION GENE FOR LIGAND BINDING

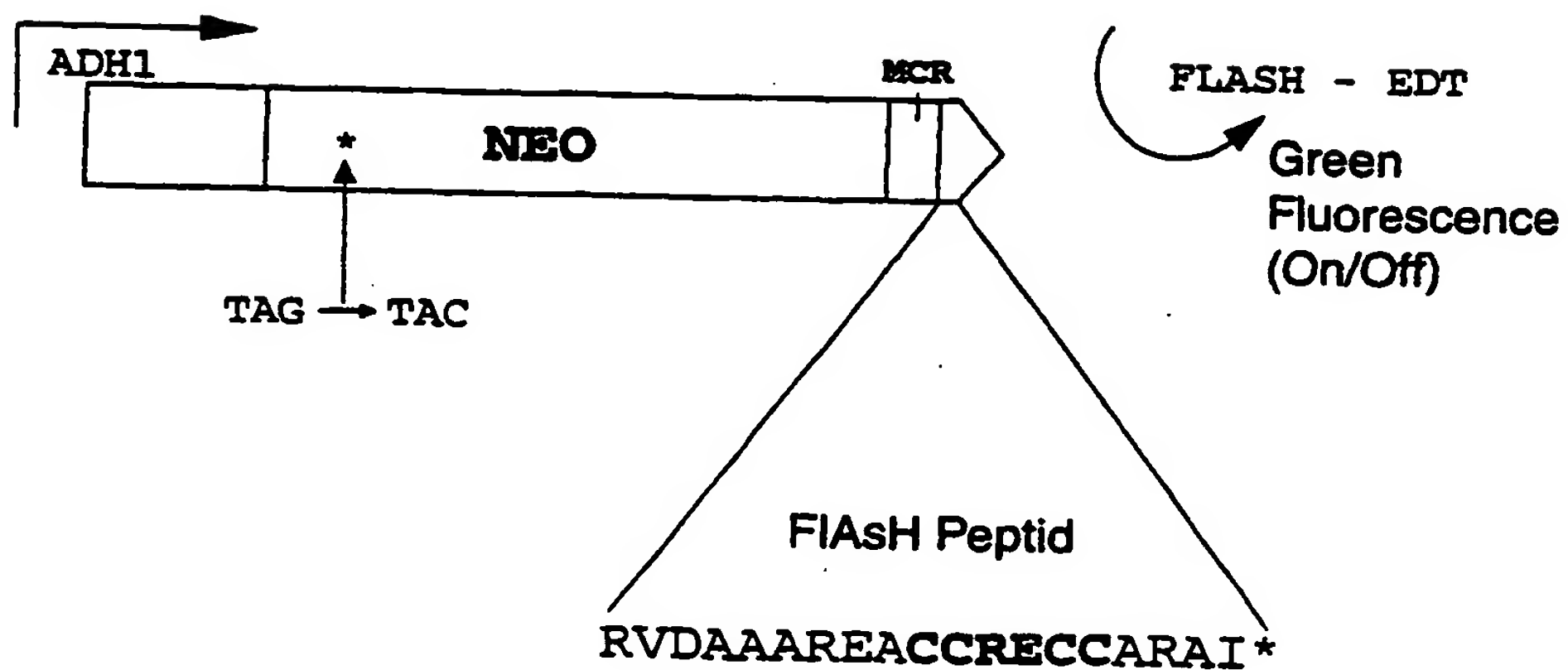


Figure 9

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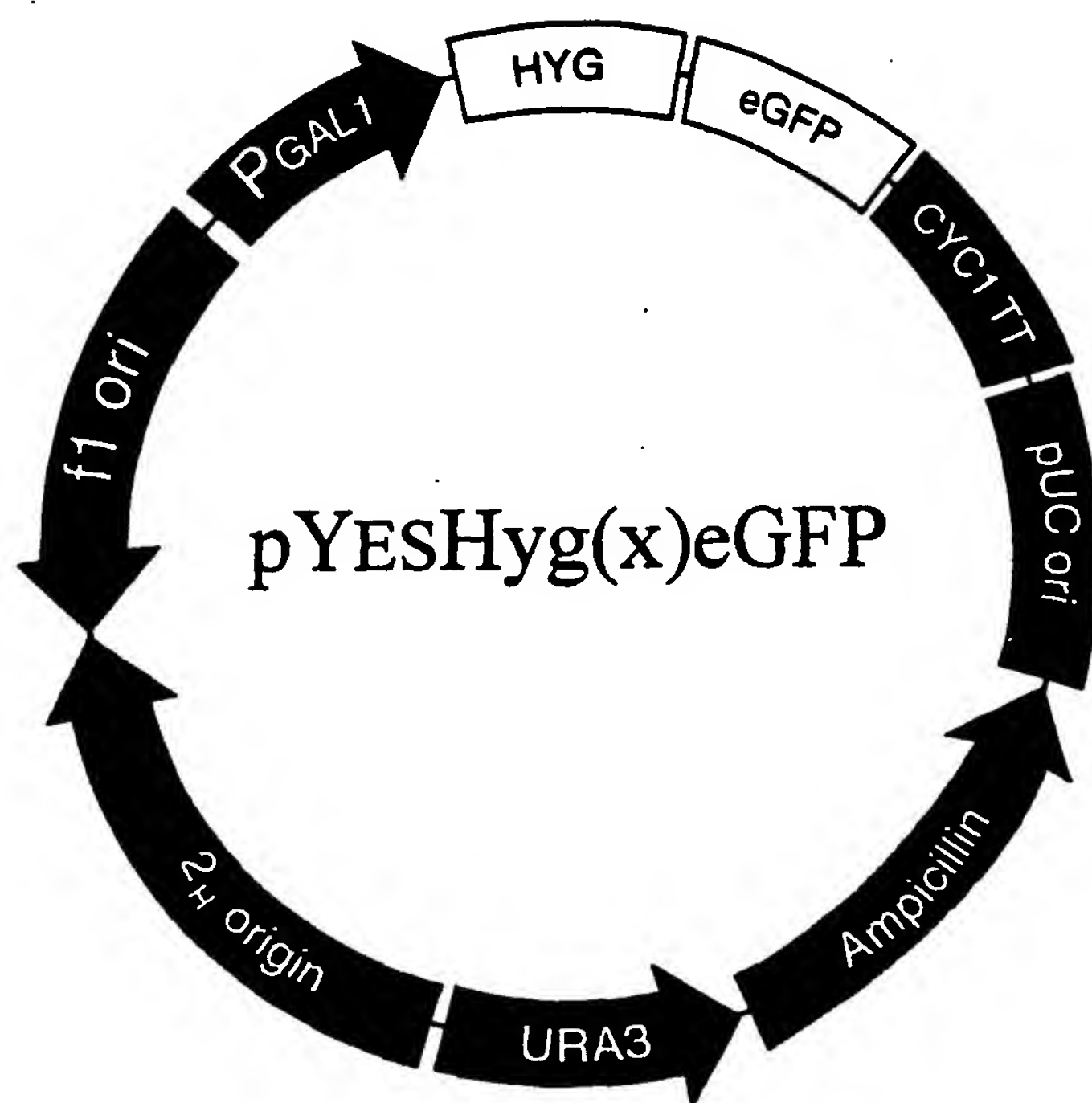


Figure 10

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International Bureau**



(43) International Publication Date
4 October 2001 (04.10.2001)

(10) International Publication Number
WO 01/073002 A3

PCT

(51) International Patent Classification⁷: C12N 15/10,
15/11, C07H 21/04, A61K 48/00, 31/7088, C12N 5/10,
A01K 67/027

B. [US/US]; 18 Crossan Court, Landenberg, PA 19350 (US). GAMPER, Howard, B. [US/US]; 904 Locust Street, Philadelphia, PA 19107 (US). RICE, Michael, C. [US/US]; 802 Washington Crossing Road, Newtown, PA 18940 (US).

(21) International Application Number: PCT/US01/09761

(22) International Filing Date: 27 March 2001 (27.03.2001)

(74) Agents: HALEY, James, F., Jr. et al.; c/o Fish & Neave, 1251 Avenue of the Americas, New York, NY 10020 (US).

(25) Filing Language: English

(26) Publication Language: English

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60/208,538	1 June 2000 (01.06.2000)	US
60/244,989	30 October 2000 (30.10.2000)	US

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(71) Applicant (for all designated States except US): UNIVERSITY OF DELAWARE [US/US]; 210 Hullihen Hall, Newark, DE 19716 (US).

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

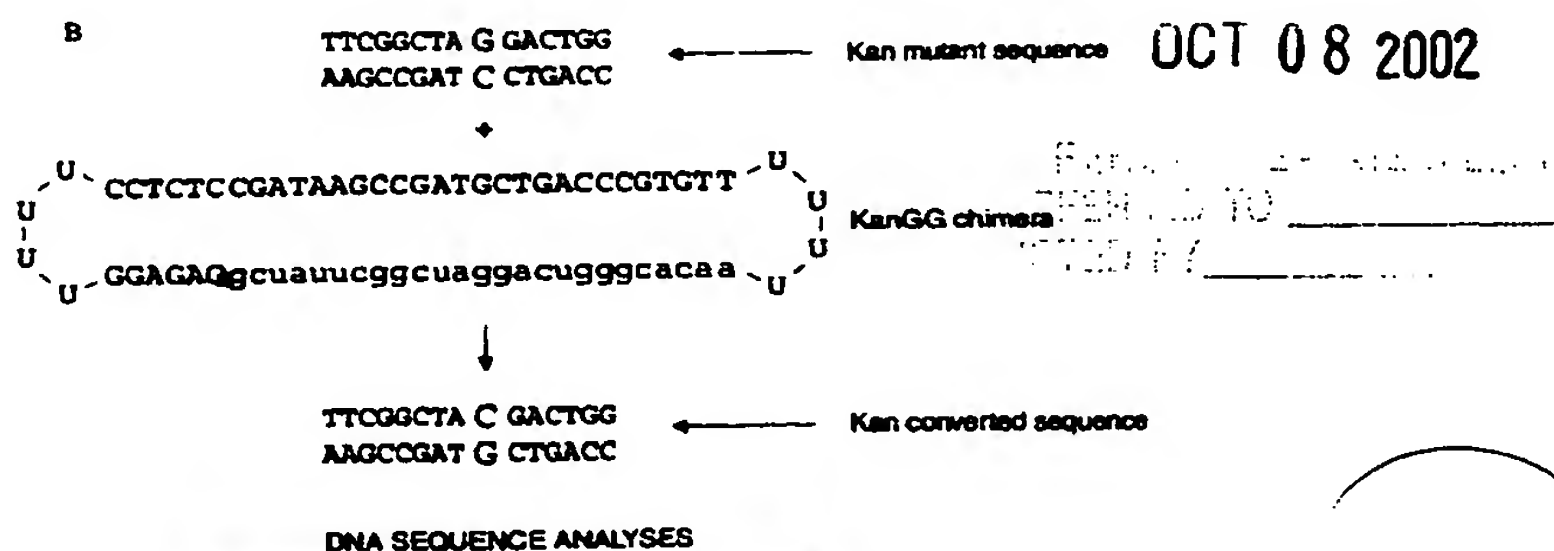
(72) Inventors; and

(75) **Inventors/Applicants (for US only):** **KMIEC, Eric,**

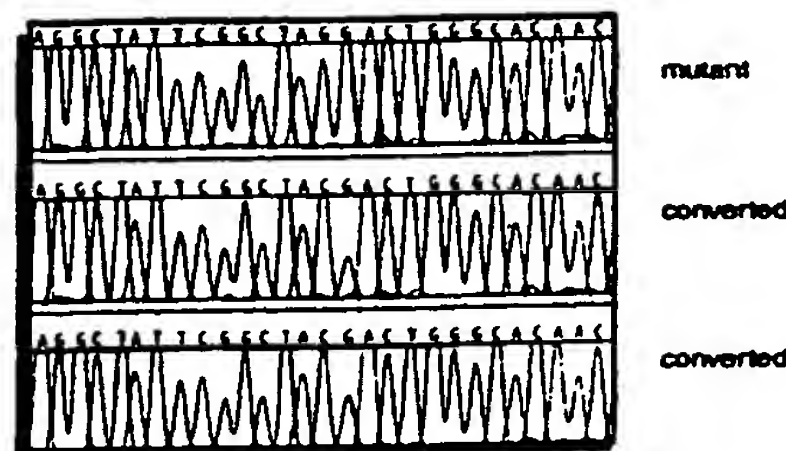
[Continued on next page]

(54) Title: TARGETED CHROMOSOMAL GENOMIC ALTERATIONS WITH MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

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DNA SEQUENCE ANALYSES



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(57) Abstract: Presented are methods and compositions for targeted chromosomal genomic alterations using modified single-stranded oligonucleotides. The oligonucleotides of the invention have at least one modified single-stranded oligonucleotides. The oligonucleotides of the invention have at least one modified nuclease-resistant terminal region comprising phosphorothioate linkages, LNA analogs or 2'-O-Me base analogs.

WO 01/073002, A3

**Declarations under Rule 4.17:**

- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG)

- as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:

26 September 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/09761

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/10 C12N15/11 C07H21/04 A61K48/00 A61K31/7088
C12N5/10 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EP0-Internal, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WOOLF T M ET AL: "TOWARD THE THERAPEUTIC EDITING OF MUTATED RNA SEQUENCES" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 92, 1 August 1995 (1995-08-01), pages 8298-8302, XP000574995 ISSN: 0027-8424	1-3,5,6, 9,10, 13-15, 19-24
Y	the whole document --- -/--	1-24

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
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Date of the actual completion of the international search

7 March 2002

Date of mailing of the international search report

19. 07. 2002

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ANDRES S.M.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/09761

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SANTISTEBAN INES ET AL: "Three new adenosine deaminase mutations that define a splicing enhancer and cause severe and partial phenotypes: Implications for evolution of a CpG hotspot and expression of a transduced ADA cDNA." HUMAN MOLECULAR GENETICS, vol. 4, no. 11, 1995, pages 2081-2087, XP002192326 ISSN: 0964-6906 the whole document	7
P,Y	--- GAMPER HOWARD B JR ET AL: "A plausible mechanism for gene correction by chimeric oligonucleotides." BIOCHEMISTRY, vol. 39, no. 19, 16 May 2000 (2000-05-16), pages 5808-5816, XP002192327 ISSN: 0006-2960 cited in the application the whole document	1-3,5,6, 8-18
Y	--- WO 99 58702 A (KIMERAGEN INC) 18 November 1999 (1999-11-18) the whole document	19-24
Y	--- WO 99 14226 A (WENGEL JESPER ;EXIQON A S (DK); NIELSEN POUL (DK)) 25 March 1999 (1999-03-25) abstract page 56, line 16 - line 30 page 149; example 131 page 168 -page 173; examples 151,152 claims 93-108	2-5
X	--- CULVER KENNETH W ET AL: "Correction of chromosomal point mutations in human cells with bifunctional oligonucleotides" NATURE BIOTECHNOLOGY, vol. 17, no. 10, October 1999 (1999-10), pages 989-993, XP002151266 ISSN: 1087-0156 cited in the application the whole document	1-3,5, 10-15, 19,22-24
A	--- CAMPBELL C R ET AL: "HOMOLOGOUS RECOMBINATION INVOLVING SMALL SINGLE-STRANDED OLIGONUCLEOTIDES IN HUMAN CELLS" THE NEW BIOLOGIST, vol. 1, no. 2, November 1989 (1989-11), pages 223-227, XP002933043 ISSN: 1043-4674 cited in the application the whole document	7
X	--- CAMPBELL C R ET AL: "HOMOLOGOUS RECOMBINATION INVOLVING SMALL SINGLE-STRANDED OLIGONUCLEOTIDES IN HUMAN CELLS" THE NEW BIOLOGIST, vol. 1, no. 2, November 1989 (1989-11), pages 223-227, XP002933043 ISSN: 1043-4674 cited in the application the whole document	1,10, 12-15
	--- -/--	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/09761

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MOERSCHHELL R P ET AL: "TRANSFORMATION OF YEAST WITH SYNTHETIC OLIGONUCLEOTIDES" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 85, January 1988 (1988-01), pages 524-528, XP002933044 ISSN: 0027-8424 the whole document ---	1,10, 13-15
X	US 5 955 363 A (LEWIS MARTIN K ET AL) 21 September 1999 (1999-09-21) column 9, line 42 -column 10, line 31 claims; examples 5,6 ---	1,13,14
A	KMIEC ERIC B ET AL: "Targeted gene repair in mammalian cells using chimeric RNA/DNA oligonucleotides." COLD SPRING HARBOR MONOGRAPH SERIES, no. 36, 1999, pages 643-670, XP001064041 ISBN: 0-87969-528-5 ---	
A	ORUM HENRIK ET AL: "Detection of the factor V Leiden mutation by direct allele-specific hybridization of PCR amplicons to photoimmobilized locked nucleic acids." CLINICAL CHEMISTRY, vol. 45, no. 11, November 1999 (1999-11), pages 1898-1905, XP002192328 ISSN: 0009-9147 the whole document ---	4,5
P,X	GAMPER HOWARD B ET AL: "The DNA strand of chimeric RNA/DNA oligonucleotides can direct gene repair/conversion activity in mammalian and plant cell-free extracts." NUCLEIC ACIDS RESEARCH, vol. 28, no. 21, 1 November 2000 (2000-11-01), pages 4332-4339, XP002192329 ISSN: 0305-1048 cited in the application the whole document ---	1-3,5,6, 8-15, 17-24
P,X	WO 01 15740 A (VALIGEN US INC) 8 March 2001 (2001-03-08) the whole document ---	1-3,5,6, 8-18
E	WO 01 92512 A (KIM JUNGSUP ;UNIV DELAWARE (US); GAMPER HOWARD B (US); KMIEC ERIC) 6 December 2001 (2001-12-06) the whole document ---	1-24

-/--

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/09761

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	<p>RICE MICHAEL C ET AL: "The potential of nucleic acid repair in functional genomics." NATURE BIOTECHNOLOGY, vol. 19, no. 4, April 2001 (2001-04), pages 321-326, XP002192330 ISSN: 1087-0156</p> <p>---</p>	
T	<p>LIU LI ET AL: "In vivo gene repair of point and frameshift mutations directed by chimeric RNA/DNA oligonucleotides and modified single-stranded oligonucleotides." NUCLEIC ACIDS RESEARCH, vol. 29, no. 20, 15 October 2001 (2001-10-15), pages 4238-4250, XP002192331 ISSN: 0305-1048</p> <p>-----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/09761

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 8,10,12 (as far as in vivo methods are concerned) and claims 11,17 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-24 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. : Claims 1-24 (all partially)

Single-stranded oligonucleotides (SEQ IDs 1 to 4) for targeted alteration of the adenosine deaminase Gln3TER mutation; modified forms thereof; compositions and kits comprising them; methods for their optimisation.

Inventions 2. to 40. : Claims 1-24 (all partially)

As for subject 1., but relating respectively to the additional ADA mutations as listed in Table 10.

Inventions 41. to 61. : Claims 1-24 (all partially)

As for subject 1., but relating respectively to the mutations occurring in the target genes of examples 5 to 25.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/09761

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9958702	A	18-11-1999	US 6010907 A 04-01-2000
		AU 740702 B2 15-11-2001	
		AU 3901499 A 29-11-1999	
		CA 2328477 A1 18-11-1999	
		CN 1309717 T 22-08-2001	
		EP 1078097 A1 28-02-2001	
		JP 2002514434 T 21-05-2002	
		WO 9958702 A1 18-11-1999	

WO 9914226	A	25-03-1999	AU 9063398 A 05-04-1999
		CA 2303299 A1 25-03-1999	
		CN 1279687 T 10-01-2001	
		WO 9914226 A2 25-03-1999	
		EP 1015469 A2 05-07-2000	
		NZ 503765 A 26-04-2002	
		US 2002068708 A1 06-06-2002	

US 5955363	A	21-09-1999	NONE

WO 0115740	A	08-03-2001	US 6271360 B1 07-08-2001
		AU 7076700 A 26-03-2001	
		BR 0013590 A 07-05-2002	
		EP 1210123 A1 05-06-2002	
		WO 0115740 A1 08-03-2001	

WO 0192512	A	06-12-2001	AU 4948801 A 08-10-2001
		AU 6527701 A 11-12-2001	
		WO 0173002 A2 04-10-2001	
		WO 0192512 A2 06-12-2001	
		AU 7906901 A 13-02-2002	
		WO 0210364 A2 07-02-2002	
